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AC116551.1 GI:19807784
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AJ132435 Arabidops
AL122103 Homo sapi
AX008675 Sequence
BC002205 Mus muscu
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AX358735 Sequence
U54559 Homo sapien
BC024504 Mus muscu
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AF060912 Macaca fa
X98928 A.thaliana
AY80737 Homo sapi
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AY80738 P.polycepha
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strain AX4,
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                   Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                         Strausberg, R.
Direct Submission
                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1455)
                                                                                                                                                                                                                      Homo sapiens
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Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 52514)

Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., I
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R.,
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A.
contact: amadan@systemsbiology.org
                                                                                                                                                                                                                                                          BC009883.1 GI:14602735
                                                                                                                                                                                                                                                                                          BC009883 1455 bp mRNA linear I
Homo sapiens, Similar to RIKEN cDNA 2600016L03 gene,
                                                                                                                                                                                                                                                                                IMAGE:3959548,
                                                                                                                                                                                                                                                                                                                                                                                                                 h 4.9%; So Similarity 100.0%; F 42; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agency: Deutsche Forschungsgemeinschaft (DFG).

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is available from IMB Jena, Department of Genome Analys: (http://genome.lmb-jena.de/dictyostellum/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostellum/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneralD may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
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                                                                                                                                                                                                                                                                                            clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dear, P.,
Kumpf, K.,
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REFERENCE
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
AX317981
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Matches 41
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                                 823
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                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl.gov Series: IRAL Plate: 25 Row: m Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                             Kearney,
Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Greene, Mark Ketteman and Anuradha Madan
                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          passed the following selection criteria: Hexamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 from Patent AX317981
                                                                                                                                                                                                                                                                                                Yue, H., Sanjanwala, M.S., Baughn, M.R., Gandhi, A.R., Ring, H.Z., Elliott, V., Walla, N.K., Yang, J., Khan, F.A., Ramkumar, J., Tang Hafalla, A., Lal, P., Nguyen, D.B., Yao, M.G., Lee, E.A., Tribouley, C.M., Patterson, C., Lu, Y., Ding, L., Bruns, C.M. and
                                                                                                                                                                                                                                                  Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX317981.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 4.8%; So Similarity 100.0%; 141; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
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                                                                  Conservative
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/protein_id="AAH09883.1"
/db_xref="G1:14602736"
/db_xref="G1:14602736"
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PVYHLCQPCAVHYDFVGSYERLEADANQVLEWVRAPPHVRFPARQAWYRPASPESLHY
HLCSAPRALLQDVLPKYYLDFSLFAYPLPNVTKEACQQ"
                                                                                                                                                                                                                                                                  WO 0190334-A 21 29-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Placenta,
/clone_Tib="NIH_MGC_21"
/lab_host="DH10B-R"_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                               /organism="Homo sapiens"
/db xref="taxon:9606"
/note="Incyte ID No: 2779244CB1"
/note="Incyte ID 92 439 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pOTB7"
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                                                           100.0%; PI
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Primates;
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; Pred. No. 2.4e-11;
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Pred. No.
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: WO0190334.
                                                                  Mismatches
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                                                                                DB 6; Le . 2.3e-11;
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                                                                  Indels
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AB079606/c
LOCUS
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A91160
LOCUS
DEFINITION
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Best Local 9
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                                                                                                                                                                                      Dictyostelium discoideum Dd-gdcA gene, AB079606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gp64 and disintegrin-like; cysteine-rich
Dictyostelium discoideum (strain:AX2) DN
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-FEB-2002) Naohisa Takaoka, Yamaguchi University, School of Medicine; 1-1-1, Minami-kogushi, Ube, Yamaguchi 755-
Japan (B-mail:ntaka@yamaguchi-u.ac.jp, Tel:81-836-22-2227,
                                                           Sequence
A91160
A91160.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takaoka, N., Hirashima, M., Fukuzawa, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene expression of a gp64 and protein of the cellular slime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takaoka, N., Fukuzawa, M., Hirashima, M., Saito, T., Maeda, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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                                                                                                                                                                                                                                                   41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                             Zea mays.
                                                                                                         A91160
                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                775
                                                                                                                                                                                                                                                   larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/proteIn_id="BAB84682.1"
/proteIn_id="BAB84682.1"
/db xref="GI:18652925"
/translation="MKFIYGLLALAASIVATNAQYCSIGVCVKEGENCNINNYNFTDN
/translation="MKFIYGLLALAASIVATNAQYCSIGVCVKEGENCNINNYNFTDN
SVVDITCEYGTFCPSSSVIFTPVCTKLSGLGETCGTPFTECAEPFACRSVTTTKGNLQ
TCAMPDYLGFGESCNSDYQCGNGLTCNEEIGSLKPHVICSNDGQCPFQGFCNGTNSLN
TPVQCRTLYATGAKCTRDGQCPYNNYCGAKQGDNSGDLFCQSNFNKVQGDTCSVHGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Dd-gdcA mRNA sequence
Acc#:AB079253."
join(557..672,809..1826)
                                                                                             v
                                                                                                                                                                                                                                                                                                                                                                           FVQLGSGFRYBCAATLVCQAGTCQSPQNSIPTGDCMDIANSCPSAYGSSCQCTSTSQI
ITGKCTASPFNLASNCQTSVQNLATCAIEHECPSIENIELGPDSCLMKHCRSEICDNN
NCIVQTNTCGDAPVYFVCNTPSSSSVILPSFVLLIVAIIALLF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein"
                                                                                                                                                                                                                                                                                                                                /gene="Dd-gdcA"
261 c 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="gp64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(557. .672,809. .1826)
/gene="Dd-gdcA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="Dd-gdcA"
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                                                              GI:6740195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and disintegrin-like,
                                                                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                 Score 41;
Pred. No.
                                                                                             WO9827212
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NOVEL NUCLEIC ACID MOLECULES FROM MAIZE AND THEIR PRODUCTION OF MODIFIED STARCH PAtent: WO 9827212-A 7 25-JUN-1998;

EMMERMANN MICHAEL (DE); KOSSMANN JENS (DE)
LOCALLON/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A91162.1
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1 (bases 1 to 2307)
Emmermann, M. and Kossmann, J.
MOVEL NUCLEIC ACID MOLECULES FROM MAIZE AND THEIR USE FOR THE PRODUCTION OF MODIFIES STARCH
PATENE: WO 9827212-A 5 25-UUN-1998;
EMMERMANN MICHAEL (DE); KOSSMANN JENS (DE)
LOCALIO, Qualifiers
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/translation="pdgttvyknralrtpfvksgdnstlribiddgvhaibplifde
Tonkwfknngonfovenskrigotgasgassatstlvpedlycolaytrwbrrgko
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LPEDLVQVQAYTRWEQAGKDNTPBEKOLVEFEBARKELQAEVDKGISIDOLROKILKG
NIESKVSKQLKNKKYFSVERIQRKKRDITQLLSKHKHTVMEDKVEVVPKQPTVLDLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / CTAINS 1 & TON = HELGGILEARVELRPILLDSRERWEDLIFLDIALDSTERTAIER
/ CTAINS 1 & TON = HELGGILEARVELRULALSIDDNEDILYCLKGWNQALEMAKQKDDQWALY
AKAFLDRIRLALSKEGQYHNMYQPSAEYLGSILSIDQWAVNIFTEEIIRGGSAATLS
ALLMREDPUTLRIVVAHLGSWQYLSPYEVEGGYVUVUDELLAVQNISYDKPTILVAKSVKG
EEEIPDGVVGVITPDMPDVLSHVSVRARNSKVLFATCFDHTTLSELEGYDQKLFSFKP
TSADITYREITESELQQSSSPNAEVGHAVPSISLAKKKFLGKYAISAEFSEEMVGAK
SRNIAYLKGKVPSWVGVPTSVAIPFGTFEKVLSDGLKKWAGSTEKLKIRLAGEDFSA
LGBIRKVVLNLTAPMQLVINELKERMLGSGMPNPGDEGDKKWAGSTEKLKIRLAGEDFSA
LGBIRKVVLNLTAPMQLVINELKERMLGSGMPNFODEGDKSBEIYAEVVKGLGET
LVGAYPGRAMSFVCKKDDLDSPKLLGYDSKPIGLIFTENDSNGEDLEGYAGAG
LVGAYPGRAMSFVCKKDDLDSPKLLGYDSKPIGLIFTENDSNGEDLEGYAGAG
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/db_xref="GI:6740198"
                                                                                                                                                                                                                    /db_xref="taxon:4577"
<2. .4012
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DGKIYVVQTRPQM"
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/db_xref="taxon:4577"
<33. .1946
                                                                                                                                                                                         note="unnamed protein product"
                                                                                                                                                                                                                                                                 organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:6740197
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/protein_id="CAB69412.1"
/db_xref="GI:6740196"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="unnamed protein product"
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Pred. No.
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. 2.3e-11;
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DEFINITION ACCESSION VERSION BASE COUNT Query Match
Best Local Similarity
Matches 41; Conserv Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to FIL CDNA.

Drosophila melanogaster

Drosophila melanogaster

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Rephydroidea; Drosophilidae; Drosophila;

Ephydroidea; Drosop vi,C., Lewis,S.E., Rubin,G.M. and Celniker,S.

Direct Submission
Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory Drosophila melanogaster GH16672 AY051514 AY051514.1 1349 a 4.8%; Scilarity 100.0%; P KSLHEKDGCEVLSRKLFKFGDKEILAISTKVQNKTEVHLATNHTDPLILHWSLAKNAG EWKAPSPNILFSGSTLLDKACETEFTKSELDGLHYQVVEIELDDGGYKGMPFVLRSGE TWIKNNGSDFFLDFSTHDVRNIKAILKDNGDAGKGTSKALLERIADLEEDAQRSLMHR VVKDGKIYVVQTRPQM" GAGLYDSVPMDEEDEVVLDYTTDPLIVDRGFRSSILSSIARAGHAIEELYGSPQDVEG GI:15291338 791 c 1048 g Score 41; DB 6; Long Pred. No. 2.1e-11; 0; Mismatches 0; 1141 t mRNA linear full length cDNA. 0, Length 4329; Indels INV 27-AUG-2001 0; 0

FEATURES

COMMENT

JOURNAL

REFERENCE

AUTHORS

SOURCE ORGANISM

KEYWORDS

RESULT 7 AY051514

Snoo

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4267

ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramur
Sequencing Center (NISC),
                                                                                                                                                                                                                                                Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC025672 2472 bp mRNA linear PRI 11-MAR-200 Homo sapiens, Similar to folate hydrolase (prostate-specific membrane antigen) 1, clone MGC:34488 IMAGE:5202715, mRNA, complete
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2472)
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
                                                                                                                                                                                                 USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                      Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      BC025672.1 GI:19343603
                                                                                Gaithersburg, Maryland;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%; Score 40; ilarity 100.0%; Pred. No. Conservative 0; Minn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="91F9-91F10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Longest ORF"
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/db_xref="FLYBASE:FBgn0025680"
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AX344799/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Series: IRAN Plate: 49 Row: e Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4758397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A. Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
AX344799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through
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                                                                                                                                                                              Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with development genes Patent: WO 0200927-A 224 03-JAN-2002;
                                                                                                                                                                                                                                                                                                    synthetic construct.
                                                                                                                                                          Epigenomics AG (DE)
                                                                                                                                                                                                                                                                            artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                      AX344799.1 GI:18492685
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SSNEATNITPSCHAMKAFLDELKAENIKKFLYRUTQIPHLAGTEROMFQLAKQIGSGWKE
FGLDSVELAHYDVLLSYPKKTHPNYISIINEDGMIFINTSLFEPPPPGYENVVSDIVPP
FSAFSPGOMPEGDLVVVNYARTEDFFKLERDWKINCSGKIVIARYGKVFKGNKVKNAQ
LAGAKGVILYSDPADYFAPGYKSYPDGWNLPGGGVORRONLINLAGAGDPLTPGYPANE
YAYRRGIAEAWGLPSIPVHPIGYYDAQKLLEKMGGSAPPDSSWRGSLKVPYNVGPGFT
GNESTGOKYMHIHSTYNEVTRIVNIGTHLAGAWEPDRYVILGGHADSWVFGGIDPGSGA
AVVHEIVRSFGTLKKEGWFPRRTILFASWDAEEFGLLGSTEMAEENSRLAGERGVAYI
NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSDDEGFEGKSLYESWTKKSPSPEFSG
MPRISKLGGSNHPESUFFGRLGIASGRAYTKNWETNKRSGYPLYHSVETYFLVEKFY
DPMFKYHLTVAQVRGGWVFELANSIVLFPDCRDYAVVLRKYADKIYSISMKHPQEMKT
YSVSFDSLFSAVKNFTSIASKYSERLOPDFXSKHVIYAPSSHNKXAGESFFGIYDALF
YSVSFDSLFSAVKNFTSIASKYSERLOPDFXSKHVIYAPSSHNKXAGESFFGIYDALF
YSVSFDSLFSAVKNFTSIASKYSERLOPDFXSKHVIYAPSSHNKXAGESFFGIYDALF
YSVSFDSLFSAVKNFTSIASKYSERLOPDFXSKHVIYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane antigen) 1"
/protein_id="AAH25672.1"
/db_xref="GI:19343604"
                                                                                                                                                                                                                                                                                                                                                                                                                      224 from Patent
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                        /organism="synthetic construct"
/db xref="taxon:32630"
/db xref="taxon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
/noTe = "chemically treated genomic DNA (Homo sapiens)"
/noTe = "chemically treated genomic DNA (Homo sapiens)"
                                                                                                               1. .10825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="MGC:34488 IMAGE:5202715"
                                                                                                                                       Location/Qualifiers
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8.1e-11;
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http://image.llnl.gov
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G38015/c
LOCUS
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Best Local Similarity
Matches 39; Conserv
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Best Local :
                                                                                                                            primer_bind
primer_bind
E COUNT
                 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
ТИТАТАТАЛААЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G38015

CLM31 Plasmodium falciparum haploid Plasmodium genomic, sequence tagged site.
G38015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Su, X.-z., Ferdig, M.T. and Wellems, T.E. Integrated genetic and physical maps of Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Machine:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tew@helix.nih.gov
Primer A: TCATCAGTACTTTCCTTGAA
Primer B: AGCTGAAGGTATGTCATAAA
STS size: 200
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G38015.2 GI:4337393
STS.
STS.
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cycles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Thomas E. Wellems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          initial heat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mar 6, 1999 this sequence version replaced gi:3077855.
                                                     4.5%; Scilarity 100.0%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 4, Room 126, NIH Campus, Bethesda, MD 20892-0425
(301) 496-4021
(301) 402-0079
                                                                                                                               66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.6%; Score 40; DB 6; Length 10825; ilarity 100.0%; Pred. No. 6.9e-11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 dNTPs:
Taq Polymerase:
Total Volume:
                                                                                                                                                                                                                                                                                                                                                                                                                       Template:
                                                                                                                                                                                                                                                                                                 50 mM KCI
                                                                                                                            complement (181.
                                                                                                                                                                   /clone_lib="plasmodium falciparum haploid"
/dev_stage="erythrocytic haploid stage"
1. .200
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                      organism="Plasmodium falciparum"
|strain="HB3xDd2"
                                                                                                                                                                                                                                                                                                           0 mM Tris HCl, pH 8.3
                                                                                                                                                                                                                          db_xref="taxon:5833"
                                                                                                                                                                                                                                                                                                                                                                                                                                            2min at 94oC
30 cycles, each having steps 20sec at 94oC;
10sec at 45oC; 10sec at 40oC; 30sec at 60oC
Perkin Elmer GeneAmp 9600
                                                     Score 39; DB 11;
Pred. No. 3.8e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                1-10 ng
5 pM each
0.3 ul of
0.5 unit
15 ul
                                                                                                                         .200)
                                                                                                                                                                                                                                                                                                                                                                                           10 mM
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                                                                                                                                                                                                                                                                                                                                                                                           stock solution
                                                                                Length 200;
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                                                       Indels
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dium falciparum
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                                                     Gaps
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um STS
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primer bind
primer_bind
BASE COUNT 1:
ORIGIN
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DEFINITION
                                        RESULT 12
AB072484
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                     Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                  108
                                                                                                            Lycopersicon cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum.
Plasmodium falciparum
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 236)
Su,X.-z., Ferdig,M.T. and Wellems,T.E.
Integrated genetic and physical maps of Plasmodium falciparum
Unpublished (1998)
Synonyms: wh hspl
Contact: Thomas E. Wellems
                          AB072484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tew@helix.nih.gov
Primer A: GCATATTATTATGAATTACC
Primer B: ATCAAAAGGTTATATATGTA
STS Bize: 236
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bldg. 4, Room 126, NIH Campus, Bethesda, Tel: (301) 496-4021
Fax: (301) 402-0079
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Wh_hspl Plasmodium falciparum haploid Plasmodium falciparum STS genomic, sequence tagged site.
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G37836
G37836.1 GI:3015442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial heat: 2min at 94oC
Cycles: 30 cycles, each having steps 20sec at 94oC;
10sec at 45oC; 10sec at 40oC; 30sec at 60oC
Machine: Perkin Elmer GeneAmp 9600
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                                                                                                                                                       4.5%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Template:
Primer:
dNTPs:
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Total Volume:
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1.5 mM MgCl2
                                                                                                                                                                                                                                                                                                                                                                                                      50 mM KCl
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                                                                                                                                                                                                                                                                    /clone_lib="plasmodium falciparum haploid"
/dev_stage="erythrocytic haploid stage"
1. .236
                                                                                                                                                                                                                                                                                                                 /map="9"
                                                                                                                                                                                                                                                                                                                                             organism="Plasmodium falciparum"
|strain="HB3xDd2"
                                                                                                                                                                                                                                                                                                                               db_xref="taxon:5833"
                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
    415 bp mRNA linear PLN 19-JUN-20 chmielewskii LcwHT-A gene for HT-A protein, partial
                                                                                                                                                       0,
                                                                                                                                                                   Score 39;
Pred. No.
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5 pM each
0.3 ul of
0.5 unit
15 ul
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                                                                                                                                                        Mismatches
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                                                                                                                                                                   DB 11;
3.7e-10;
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                                                                                                                                                                               Length 236;
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                                                                                                                                                       Indels
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                                                                                                                                                     Gaps
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AUTHORS
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KEYWORDS
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AUTHORS
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ORIGIN
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KEYWORDS
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AY070797
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TITLE
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Best Local :
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TITLE
                                                                                                                                                                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                  371
                                                                                                                                                                                                                                                                                                                                                                           ТАТАТАТАВААЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА
                                                                                                                                                                                                                                                                                                                                                  TATATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
      Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Noptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 691)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,

Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,

George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,

Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,

Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.

and Celniker, S.
                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (04-OCT-2001) Yasuo Kowyama, Mie University, Faculty of Bioresources; Kamihama-cho 1515, Tsu, Mie 514-8507, Japan (E-mail:kouyama@bio.mie-u.ac.jp, Tel:81-59-231-9483,
                                                                                                                                                                                                                                 691 bp
Drosophila melanogaster AT18217
AY070797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon chmielewskii

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB072484.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insights into the evolution of self-compatibility in Lycopersicon from a study of stylar factors Plant J. 30 (2), 143-153 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hattori, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kondo, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon chmielewskii (strain:LA1316) mature pistil cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax:81-59-231-9637)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon.
                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                    AY070797.1 GI:17944700 FLI_CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                              4.5%;
larity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLFPNIACLGCSCPKKDNNNNNNNNNDDDDDDDDFIGNVCKAMCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="self-incompatibility"
/codon_start=1
/product="HT-A protein"
/protein_id="BAC00944.1"
/db_xref="GI:21623726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, M., Itahasi, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="LcwHT-A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:62889"
/tissue_type="pistil"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="LcwHT-A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Lycopersicon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="SLVLLIISSEVIAREMVEANQVQNTFELDNPTLQKKSGGGKGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain="LA1316"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
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ORGANISM
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TITLE
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Best Local
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BC028785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cdna@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                    Mus musculus, clone IMAGE:1246046,
                                                                                                                                                           Direct Submission
                                                                                                                                                                           Strausberg, R
                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                      house mouse
                                                                                                                                                                                                                                                                                                                                        BC028785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="AT18217p"
/protein_id="AAL48419.1"
/db_xref="GI:17944701"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Drosophila"
/db_xref="taxon:7227"
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Pred. No.
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes for further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: Soares Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                             Submitted (29-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 988)
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39; Conservative
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Submitted (18-FEB-2000) IMPI, C
University Hospital, Stockholm
Location/Qualifiers
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1121)
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ob_xref="taxon:9606"

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clone_lib="Soares_mammary_gland_NbMMG"

lab_host="DH10B"
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TRLSRRVLRDISERGRDLEQILSQYITFVKFAFEEFCLFTKKYADVII-PRGADNLVAI
NLIVOHLODILNGEPSRKEQTNGCLNGYTFSRKKQASESSSRPH"
a 281 c 268 g 242 t
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밁 Ś Best Local Si Matches 39; Query Match 1075 ТАТАТАТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 1113 Similarity 4.5%; Score 39; DB 9; Length 1121; ilarity 100.0%; Pred. No. 3.1e-10; Conservative 0; Mismatches 0; Indels 0 Gaps

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15-JUN-2000;
22-JUN-2000;
                                                                         hyperplasia, Cushing's disease, endometriosis, infertility, hypergonadal disorders, and gynaecomastia. Eye disorders include conjunctivitis, keratitis, glaucoma and macular degeneration, and metabolic disorders include diabetes, cystic fibrosis, goitre, hypercholesterolaemia, hypoglycaemia, hyperlipidaemia, lysosomal storage diseases, obesity, phenylketonuria and hypocalcaemia. Also the molecules are useful for treating gastrointestinal disorders such as dysphagia, gastritis, peptic ulcer, cholelithiasis, cirrhosis, hepatitis, hyperbilitribinaemia, constipation, diarrhoea, jaundice, Wilson's disease, thrombosis and hepatic tumours. The DME polypeptide is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walia NK,
Nguyen DB,
Burford N,
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and gastrointestinal disorders, including liver disorders. The autoimmune/inflammatory disorders treatable include AIDS, adult respiratory distress syndrome, Addison's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is human drug metabolising enzyme (DME)-8 DME polypeptide, polynucleotide and modulators are useful for diagnosis, treatment and prevention of autoimmune/inflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human drug metabolizing enzymes and polynucleotides encoding the enzyme for diagnosing, preventing or treating cell proliferative, autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis, treatment and prevention of autoimmune/inflammator cell proliferative, developmental, endocrine, eye, metabolic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2001
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     2037
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Yao MG,
Ding L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000US-207901P.
; 2000US-208983P.
; 2000US-209861P.
; 2000US-211825P.
; 2000US-213744P.
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     B₽;
                                                   agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a MS, L,
J, Khan FA, Tr'
Lee EA, Tr'
427 A; 589 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INC.
                                                      antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nn MR, Gandhi AR, Ring HZ
Ramkumar J, Tang YT, Ha
Tribouley CM, Patterson
M, Kearney L, Reddy R;
  582 G;
439 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HZ, Elliott V;
Hafalia A, Lal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ú
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RESULT 2
AAV44318
ID AAV44318
AC AAV4
XX AAV4
XX AAV4
XX AAV4
XX AAV4
CO CO COCO
RESULT 3
AAV44319
ID AAV4
XX
AC AAV4
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DT 07-C
DT 07-C
DE Seq
XX
EW Star
KW tran
XX
OS Unkr
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Best Local S
Matches 41
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes a novel maize starch-associated protein that occurs both bound to starch grains and in soluble form in plant cells. Such a protein can be used to produce transgenic plants or plant cells which are capable of synthesising modified starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding maize starch-associated protein in potatoes corresponding protein, vectors, transgenic plants, antibo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize starch-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                           2201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1996;
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  Unknown
                                                transgenic
                                                                       Starch-associated protein; maize; starch grain; soluble;
                                                                                                                     Seq ID #7
                                                                                                                                                                       07-OCT-1998
                                                                                                                                                                                                                     AAV44319;
                                                                                                                                                                                                                                                                 AAV44319 standard; DNA; 4329 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2307 BP; 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 43-46; 55pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998-349465/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                       PLANTTEC
                                                                                                                       from DE196533176.
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                                                plant;
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                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kossmann
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/product= "starch-associated protein"
/note= "no start codon given"
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ss.
                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.8%; Score 41; DB 100.0%; Pred. No. 2. tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 436 C; 555 G; 623 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ū
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19; ...
o. 2.4e-06; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT 4
ABN8027/c
ID ABN802
XX ABN802
XX ABN802
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XX Human
XX Human
XX Human
XX Human
XX Homo s
OS Homo s
OS Synthe
XX WO2002
XX O2-JUN
PR 30-JUN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; developme heart disease; edwarfism; single antidiabetic; cy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This specification describes potato and maize starch-associated proteins that occur both bound to starch grains and in soluble form in plant cells. Such a protein can be used to produce transgenic plants or plant cells which are capable of synthesising modified starch.

NOTE: This sequence is not described or represented in the specification but is presented in the sequence listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding maize starch-associated protein in potatoes corresponding protein, vectors, transgenic plants, antibo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4329 BP; 1349 A; 791 C; 1048 G; 1141 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page -; 55pp; German.
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                                                WPI; 2002-130908/17.
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01-SEP-2000; 2000DE-1043826
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les 41; Conservative
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                                                                                                                                                 EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 10825
                                                                                                 Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ease; epilepsy; histone deacetylation;
single nucleotide polymorphism; SNP; of
tic; cytostatic; anticonvulsant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                   Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOX; diabetes; cancer; apoptosis;
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0

Novel nucleic acid useful for diagnosis and therapy of

diseases

disorders

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RESULT 5
AAI80550
ID AAI8
AX AAI8
XX AAI8
XX AAI8
XX AAI8
XX AAI8
XX Hum
XX Hum
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XX Neis
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CC Note: The sequence data for this patent did not form part of the printed CC specification but is based on sequence information supplied to berwent by CC the European Patent Office.
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Best Local S
Matches 40
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                           28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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Best Local
                                                                                                         Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                        01-SEP-2001; 2001WO-EP10074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                  cell differentiation;
                                                                                12; 56pp + Sequence Listing; 56pp;
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format
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This invention describes a novel method for determining the degree methylation of a particular cytosine in a motif 5'-CpG-3', present genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the gent DNA that contains the target C is amplified to form a labeled ampli

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member, of oligonuclear and/or peptide-nucleic acid (PNA) oligomers can determine the amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The method cisses of oligoners, the degree of methylation is calculated. The method cis used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Cabolishop the degree of cytosine methylation described in the cutoff of determining the degree of cytosine methylation described in cross the invention.
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genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the
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05-SEP-2000;
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                                                                                                                       This invention describes a novel method for determining the degree methylation of a particular cytosine in a motif 5'-CpG-3', present
                                                                                                                                                                           Claim 12;
                                                                                                                                                                                                                                              Determining the degree of cytosine methylation in
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hybridization
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Matches 39
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

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                                                                                                                                                                                                                                                 Tang YT,
Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1061 BP;
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Wang Z,
Zhou P,
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ilarity 100.0%;
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Wehrman T, X
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCDN, ADDN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with
                                                                                                                                                                                                                                               Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes ass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; anti-HiV; anticonvulsant; ophthalmological; anti-Hivitic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, as primer oligonucleotides and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs).

Note: The sequence data for this patent did not form part of the printed specification but it based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
01-SEP-2000;
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ABL32875
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The present invention provides a number of human immune system associa genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

immune system associated ytosines. The sequences

Claim 1;

SEO

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848;

32pp +

Sequence

Listing;

German

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RESULT 11
ABL32763/c
ID ABL3277
XX ABL327
XX ABL327
XX ABL327
XX Human
XX Human;
KW Human;
KW antiar
KW neurop
KW antiin
KW antiin
KW antiin
KW Gene;
XX Homo s
PN W02002
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CCC Genes
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Query Match
Best Local &
Matches 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; optibaloscical; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; antipsoriatic; antientiammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5273 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune
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                                                                                                  macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                               The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, can be used in the diagnosis and treatment of immune system disorders, can be used in the diagnosis and treatment of immune system disorders, can be used in the diagnosis and treatment of immune system and including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                         Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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 1 Similarity 39; Conserv
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                                                                    5313
                                                                                                                                                                                                                                                       SEQ ID NO 736; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
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   Conservative
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2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                    BP;
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                                                                  1449 A; 70
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Pred. No.
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                   Score 39;
Pred. No.
                                                                    C; 1156 G;
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     Mismatches
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                                                                      2638 T;
                                   DB 24;
                   1.2e-05;
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                                    Length 5313;
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863

Query Match Best Local S Matches 39

Similarity

4.5%;

Score 39; Pred. No. Mismatches

DB 24; 1.1e-05;

Length 6120;

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6120

BP;

1312 A; 113 C; 1427 G; 3268 T; 0 other;

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Conservative

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ID ABN80302/s
AC ABN80302;
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                                                     The invention relates to a nucleic acid (I) comprising a sequence at CC least 18 bases in length of a segment of chemically pretreated DNA (II) CC of genes associated with development selected from 87 genes listed in CC the specification such as ACCPN, ADRN, or AFDI and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is CC useful for the diagnosis or therapy of diseases associated with CC development genes, in particular disease related to homeobox containing CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related to CC dispomers specific to each of the genes are useful for detecting the CC oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or CC (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, (II) and/or their complements and CC single nucleotide polymorphisms (SNPs).

CC Note: The sequence data for this patent did not form part of the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes ass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 319; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-130908/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2001; 2001WO-EP07536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA; cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunclogical disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis; neurocegenerative disorder; wardenburg syndrome, Niemann-Pick disease; myelocysplastic syndrome; myocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyglutamine disorder; solid tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA transcription associated genomic DNA #157.
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06-APF-2001; 2001WO-EP03973. 06-DEC'-2001

06-APR-2000; 07-APR-2000; 30-JUN-2000; 01-SEF-2000; (EPIG-) ; 2000DE-1019058. ; 2000DE-1019173. ; 2000DE-1032529. ; 2000DE-1043826. ĄG

Piepenbrock C, Berlin

WPI; 2002-090046/12

New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid disorders, tumours or Werner syndrome, psoriasis, cancer

SEQ ID ö 313; 32pp; English.

The invention relates to a nucleic acid, which comprises a segment of the C chemically pretreated DNA of genes associated with DNA transcription from CC one of 346 sequences, and an oligomer; in particular an oligomucleotide core peptide nucleic acid (PNA)-oligomer that hybridises to or is identical CC to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the CC cytosine methylation state and/or single nucleic acids are useful for dispersion of the achemically pretreated genomic DNA. The nucleic acids are useful for CC diagnosing or treating diseases associated with DNA transcription CC (particularly with the methylation stateus), e.g. adenosine deaminase CC deficiency, viral infection, retroviral infection, Sezary syndrome, CC (particularly with the methylation status), e.g. adenosine deaminase CC (particularly with the methylation status), e.g. adenosine deaminase CC (particularly with the methylation status), e.g. adenosine deaminase CC (particularly with the methylation, postival infection, Sezary syndrome, CC (particularly with the methylation status), e.g. adenosine deaminase CC (particularly with the methylation, postival disorders, werner syndrome, CC (particularly viral infection, retroviral infection, Sezary syndrome, CC (particularly disorders, immunological disorders, werner syndrome, CC (particularly disorders, postivals, Rieger's syndrome, CC (particularly disorders, postivals, Rieger's syndrome, CC (particularly disorders, manuforgenerative disorders, waardenburg CC (particularly disorders, manuforgenerative disorders, solid tumours concerns sequences ABK28127-ABK28472 represent DNA transcription CC (particularly CC) (particularly form the specific ation but was obtained in electronic format directly from the cCC (particularly format directly from the printed specific ation but was obtained in electronic format directly from the

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                                                                                                                                                                        The invention relates to a nucleic acid comprising a sequence of at least C1 8 bases of a segment of chemically pretreated DNA of genes associated With cell signalling. The activity of the modified sequences of the C2 invention may be described as cytostatic. The object of the invention is C3 to provide the chemically modified DNA of genes associated with cell C4 city of the control of the invention is C5 city of the control of the invention is C6 city of the control of the invention is C7 city of the control o
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genom sequences of genes associated with cell signalling -
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                                                                                                                                                                   European
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01-SEP-2000;
  29-JUN-2001; 2001WO-EP07471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell signalling; cytosine methylation; cell signalling disease;
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                                                                                                                                                                      Patent
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                                              Conservative
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RESULT 15 ABN80288/c

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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a nucleic acid (I) comprising a sequence at CC least 18 bases in length of a segment of chemically pretreated DNA (II) CC of genes associated with development selected from 87 genes listed in CC the specification such as ACCPN, ADFN, or AFDI and comprising one of 350 CC useful for the diagnosis or therapy of diseases associated with CC development genes, in particular disease related to homeobox containing CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes CC associated with congenital heart disease, epilepsy, diseases related to homeobox containing CC development of the brain and limb girdle muscular dystrophy and dwarfism. CO disjoners specific to each of the genes are useful for detecting the CC methylation state of all CpG dinucleorides within the 350 sequences or CC (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, (II) and/or their complements CC as oligomer probes for detecting the cytosine methylation state and/or Sindle nucleotide solvmorphisms (NDPs).
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01-SEP-2000; 2000DE-1043826.
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Sequence 7046 BP; 1785 A; 127 C; 1669 G; 3465 T; 0 other;
                                                                                                                                                                                                                                                                                                                                               single nucleotide polymorphisms (SNPs).

Note: The sequence data for this patent did not form part of the printed specification but is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 305; 27pp; English.
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Sequence 7, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 7, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 7, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SIY-1 Sequence 1, Appli 32 3,7 1325 4 US 08-212-SI	Sequence 1, Appli 92 US-06-06-09-79 Sequence 1, Appli 92 US-06-06-09-79 Sequence 1, Appli 92 US-06-06-07-12-13 Sequence 1, Appli 92 US-06-06-07-12-13-13-13-13-13-13-13-13-13-13-13-13-13-	Sequence 1, Appli 991 991 991 991 991 991 991 991 991 99

977 979 980 981 983 983 983 988 988 988 988 999 999 1000

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Sequence 2, Application US/08706214

Patent NC. 5770720

GENERAL INFORMATION:
APPLICANT: Deul, Thomas F.
APPLICANT: Shenk, Thomas E.
TITLE OF INVENTION: UBIQUITIN CONJUCATING ENZYMES HAVING
TITLE OF INVENTION: TRANSCRIPTIONAL REPRESSOR ACTIVITY
NUMBER OF SEQUENCES:
ADDRESSEE: Paul A. Stone, Esq.
STATE: Missouri
COITY: St. Louis
STATE: Missouri
                               FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,040
FILING DATE: 21-MAY-1996
PRIOR APPLICATION NUMBER: US 60/002,995
PRILING DATE: 30-AUG-1995
ATTORNSY/AGENT INFORMATION:
NAME: Stone, Paul A.
REGISTRATION NUMBER: J8,628
REFERENCE/DOCKET NUMBER: JWH 10033
TELECOMOUNICATION INFORMATION:
TELEPHONE: (314) 231-5400
TELEPIAX: (314) 231-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 63102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          имвек: US/08/706,214
30-AUG-1996
N. F.,
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US-08-630-915A-23
US-08-65-655-55-5
US-08-461-985-1
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US-08-461-985-1
US-08-461-985-1
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US-08-932-787B-1
US-08-931-0120-1
US-08-931-0120-1
US-08-931-615-2
US-08-314-615-2
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US-08-314-615-2
US-08-314-615-2
US-08-314-615-2
US-08-481-130-4
US-08-481-130-4
US-08-485-604-4
US-08-485-604-4
US-08-485-604-4
US-08-487-113D-2
US-08-487-113D-2
US-08-487-113D-2
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NAME/KEY:

LOCATION:

US-08-706-214-2
                                                                                                                                                                                                     TELEFAX: (314) 207 ITELEX: 6502697583 MCI INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: 1-ENGTH: 1356 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-08-706-214-1
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Patent No.
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,214
FILING DATE: 30-AUG-1996
CLASSIFICATION DATA:
APPLICATION WIMBER: US 60/018,040
FILING DATE: 21-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,995
FILING DATE: 30-AUG-1995
AFTING DATE: 30-AUG-1996
AFTING DATE: 30-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Deul, Thomas F.

APPLICANT: Beul, Thomas F.

APPLICANT: Shenk, Thomas E.

TITLE OF INVENTION: UBIQUITIN CONJUCATING ENZYMES HAVING TITLE OF INVENTION: TRANSCRIPTIONAL REPRESSOR ACTIVITY NUMBER OF SEQUENCES:

ADDRESSEE: PRIL A CECCA FOR THE ADDRESSEE AND RESERVE BELL A CORRESPONDENCE ADDRESS:
                                                                         MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1100 ТАТАТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛ
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STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: CONA to THYPOTHETICAL: NO
                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: 1
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                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: 111
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ZIP: 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Paul A. Stone, Esq.
STREET: One Metropolitan Square, 16th Floor
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Sim
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5. 5770720
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Similarity 100.0%;
37; Conservative (
CDS
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RESULT 1 US-08-706-214-2

COUNTRY:

USA

1137 base pairs

US-08-706-214-1

Length 1856;

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RESULT 3
US-07-642-002-1/c
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; Patent No. 5268465
; GENERAL INFORMATIO
APPLICANT: Bred
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                                                                                                                              US-07-642-002-1
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Best Local
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                                                             Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNNY/AGENT INC.

NAME: Kagan, Sarah A.

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 1107.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 296-7830

TELEFAX: (202) 296-7830

TELEFAX: (202) 296-7830
                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 296-783
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            TOPOLOGY: 11near MOLECULE TYPE: cD! HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1819 ТАТАТАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION US/07/642,00
FILING DATE: 19910118
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, Randall
APPLICANT: Snyder, Solomon H.
TITLE OF INVENTION: Purification and Molecular Cloning
TITLE OF INVENTION: Oxide Synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: O
                                                                                                                                            NAME/KEY: CDS
LOCATION: 400..4686
OTHER INFORMATION:
 39
                                                                                                                                                                                                                                                                                                                             LENGTH: 5108 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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Hwang, Paul M.
Reed, Randall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Banner, Birch, McKie & Beckett
One Thomas Circle, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                         4.3%; Score 37; DB 1; Lilarity 100.0%; Pred. No. 2.2e-07; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                 linear
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100.0%; Pred. No. 2.4e-07;
tive 0; Mismatches 0;
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                                                                                              Length 5108;
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RESULT 4
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COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION UNMBER: 36,252
TELECOMOUNICATION INFORMATION:
TELEPAN: (215) 563-4100
TELEPAN: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10136 base pairs
TYDER: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-353-700-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                        Sequence 2, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: (
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: YEN, TIMOTHY J. APPLICANT: RATTNER, JEROME B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                         APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: HUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: double
                                                                                            STREET: 1601 Market
CITY: Philadelphia
                                                                               STATE:
                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19103-2307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                            Application PC/TUS9516216
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                                                                             PA
                                                                                                                E: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEIC ACID ENCODING A TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.3%; Score 37; DB 1; 1
100.0%; Pred. No. 2.1e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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; ANTI-SENSE: NO
PCT-US95-16216-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-171-156A-61
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APPLICATION NUMBER: US 08/353,
APPLICATION NUMBER: US 08/252
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (21.5) 563-4100
TELEPHONE: (21.5) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10136 base pairs
TYPH: mucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61, Application US/09171156A Patent No. 6368846 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sin
Matches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10086 ТАТАТАРАЛАРАЛАРАЛАРАЛАРАЛАРАЛАРАЛАРА 10122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11100.
MOLECULE TYPE: DNA
MOLECULE TYPE: NO
TELEPHONE: 303/863-9700
TELEPAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                 COMPUTER: IBM POPPY
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/171,156A
FILING DATE: 04-Mar-1999
CLASSIFICATION: CURKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 827 ТАТАТАААЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛ 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              ZIP: 80202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCRRESPONDENCE ADDRESS:
ADDRESSE: SHERIDAN ROSS P.C.
STREET: 1560 BROADWAY, SUITE 1200
CITY: DENVER
STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS APPARATUS TO COLLECT SUCH PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFPLICANT: Hunter, Shirley Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 4.3%; Score 37; DB 5; L4 Similarity 100.0%; Pred. No. 2.1e-07; 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eric R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/353,700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-171-156A-63/c
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                                                                                                                                       US-09-171-156A-63
                                                                                                                                                                                                                                                     MEDIUM TYPE Floppy disk
COMPUTER: LEM PC compatible
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/171,156A
FILING DATE: 04-Mar-1999
CLASSIFICATION: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: COnnell, Gary J.
REGISTRATION NUMBER: 2618-17-C4-PUS
REGISTRATION INVBER: 2618-17-C4-PUS
TELEPHONE: 303/863-9700
TELEPAX: 303/863-973
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 63, Application US/09171156A Patent No. 6368846 GENERAL INFORMATION:
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Best Local Similarity
Matches 36; Conserv
                                                                                                   Query Match
                                                                    Matches
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                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS P.C.
STREET: 1560 BROADWAY, SUITE 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weber, Eric R.
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hunter, Shirley Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                    36;
                                                                                   Similarity
                                                                                                                                                                                                      LENGTH: 1007 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: DENVER
STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 1..465
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ilarity 100.0%;
Conservative (
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                                    4.2%; or 100.0%; Pred. No. 17re 0; Mismatches
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                                                                                 Score 36; DB 4; L
Pred. No. 6.8e-07;
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                                                                                                    Length 1007;
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RESULT 8

US-07-861-458C-37

Sequence 37,

Application US/07861458C

No.

GENERAL INFORMATION:

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1563 АТАТААЛАЛААЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 1598

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RESULT 9
5196333-3
; Patent No. 5196333
; Patent No. 5196333
; APPLICANT: CHALFIE, MARIN; WOLINSKY, EVE; DRISCOLL, MONICA
; APPLICANT: CHALFIE, MARIN; WOLINSKY, EVE; DRISCOLL, MONICA
; TITLE OF INVENTION: DNA SEQUENCES INVOLVED IN NEURONAL
; DEGENERATION, MULTICELLULAR ORGANISMS CONTAINING SAME AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ś
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                                                                                                                                                                                                     SEQ ID NO:3:
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Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION UMWEER: US/07/861,458C
FILING DATE: 04/01/92
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/014001
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marchionni, Mark Andrew
APPLICANT: Johnson, Carl D.
TITLE OF INVENTION: HOMOLOGY CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/530,968
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1563 АТАТААЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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828 ATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                             FILING DATE: 30-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                   LENGTH: 1607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617) 542-8906
                                                                    Conservative (
                                                                    4.2%; Score 36; DB 6; Le
100.0%; Pred. No. 6.5e-07;
ive 0; Mismatches 0;
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                                                                                                              Length 1607;
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; NAME/KEY: CDS
; LOCATION: (159)..(1553)
US-09-182-816-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2 Patent No.
                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/09182816 Patent No. 6143542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.2%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wishewski, Nancy
APPLICANT: Silver, Gary M.
APPLICANT: Silver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: PROTEINS AND USES THEREOF
FILE REFERENCE: FC-3-C1
CURRENT FILINGNUMBER: US/09/182,816
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/989,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEC ID NOS: 31
COMPMENDED: Defeater Ver 2 0
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TYPE: DNA
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100.0%; Pred. No. 6.5e-07
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RESULT 14
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· Sequence 22, Application US/09634530
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FINGTH: 1736
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SEQ ID NC 22
LENGTH: 1736
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CURRENT FILING DATE: 1999-12-27
EARLIER APPLICATION NUMBER: 09/182,816
EARLIER FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/989,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Silver, Gary M.
APPLICANT: Silver, Gary M.
APPLICANT: Silver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF FILE REFERENCE: FC-3-C1-1
CURRENT ELING DATE: 1999-12-27
EARLIER APPLICATION NUMBER: 09/182,816
EARLIER APPLICATION NUMBER: 09/182,816
EARLIER APPLICATION NUMBER: 09/989,510
EARLIER FILING DATE: 1998-10-29
EARLIER FILING DATE: 1997-12-12
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APPLICANT: Silver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF
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LOCATION: (159)..(1553)
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SEQ ID NO 22
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CURRENT APPLICATION NUMBER: US/09/634,530
CURRENT TILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 09/471,528
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 09/182,816
PRIOR PELICATION NUMBER: 09/182,816
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 08/989,510
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1997-12-12
RUMBER OF SEQ ID NOS: 35
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FILE REFERENCE: FC-3-C1-1
CURRENT APPLICATION NUMBER: US/09/634,530
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 09/471,528
PRIOR APPLICATION NUMBER: 09/471,528
PRIOR FILING DATE: 1999-12-27
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Patent No.
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APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF FILE REFERENCE: FC-3-C1-1
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PPLICANT: Lo, Katherine C.

PPLICANT: Brandt, Kevin S.

PPLICANT: BRANDTION: FLEA EPOXIDE HYDROLASE
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Conservative 0; Mismatches 0;
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., and Wilson, R.
                                                                                                                                                                                                                      BM732121 562 bp mRNA linear EST 01-MAR-2002 sal73B011.Y1 Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1061-4678 5' similar to TR:Q39028 Q39028 ATMYB2.;, mRNA
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                                                                     GATCCAGAAGCACATCAAGCAAGCTGAGAACTTTCAGCAACAGAGTAGTAATAATTCTGA
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         GATAAATGATCACCAAGCTAGCACTAGCCATGTTTCCACCATGGCTGAGCCCATGGAGAT
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                                                        GATCCAGAAGCACATCAAGCAAGCTGAGAACTTTCAGCAACAGAGTAGTAATAATTCTGA
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Seq primer: -40RP from Gibco
High quality sequence stop: 4
Location/Qualifiers
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1800
Fax: 314 286 1810
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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/tissue_type="mature flowers of field grown plants"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: 1-vockin@uiuc.edu

Email: 1-vockin@uiuc.edu

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call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)

call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other ESTs: AW459279 corresponding to Gm-c1016-5560 (5') Contact: Vodkin, L.O., PI, A Functional Genomics Program Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. an A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Tel: (217) 244-61
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BE820766
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                                                                                                                /clone="Time-1070-4966"
/clone lib="Gm-r1070"
/note="The library Gm-r1070 is a sequence-driven, reracked
/note="The library Gm-r1070 is a sequence-driven, reracked
/note="The library Gm-r1070 is a sequence-driven, reracked
set of 9,216 clones selected from cDNA libraries from
various tissues and stages of development of soybean that
represent 2,639 sequences from immature cotyledons, 1,770
from immature seed coats, 3,938 from flowers, and 869
from young pods. The 5' ESTs of the source clones from
the different libraries was used to select singletons, or
a representative of each contig, which were reracked to
form library Gm-r1070. The cDNA clones of the reracked
Gm-r1070 library were then sequenced at the 3' end. The
contig analysis to select unique genes was performed by
the laboratory of Ernest Retzel, Center for Computational
Genomics and Bioinformatics, University of Minnesota,
http://www.cbc.umm.edu/ResearchProjects/Soybean/index.html
Reracking was performed by Genome Systems, St. Louis,
http://www.genomesystems.com, and 3' sequencing by the
Keck Center for Comparative and Functional Genomics,
University of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detainformation on the source library for each clone can be obtained by referring to the Genome Systems clone
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                                                                                                                                                                                                       Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
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Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
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Tel: 314 286 1800
Fax: 314 286 1810
                                            Washington University School of Medicine
                                                                                                      Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                          ATGCAATTACTGAACGGTGATTAAATATTATCAAGATAAAACCTAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGAAGGACTGATAATGAGATCAAGAACTATTGGAGGACAAGGATCCAGAAGCACATC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTAGCACTAGCCATGTTTCCACCATGGCTGAGCCCATGGAGATGTATTCTCCACCCTGT
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Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                              450 bp mRNA linear EST 03-DEC-2001 sn23b01.yl Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-12290 5' similar to TR:Q9ZTD5 Q9ZTD5 PUTATIVE TRANSCRIPTION FACTOR ;, mRNA sequence.
                                                                                                                  EST
                                                                                                                                      BE058947.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145
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,lab_host="XL10-Gold"
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db_xref="taxon:3847"
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100.0%; Pr
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Pred. No. 3.3e-76;
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                                                                                                                                         TAGAGCCATTTTCAACTCAGTTCCCTACAATTAATCCTGATCAATCCATTTGTTGTACCA
                                                                                                                                                                                                                                         ATGTTTCCACCATGGCTGAGCCCATGGAGATGTATTCTCCACCCTGTTATCAAGGAATGT
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This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 411.
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Gm-c1016"
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|lab_host="XL10-Gold"
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Pred. No. 1.2e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrògen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
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Fax: 314 286 1810
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t Length: 1068 Std Error: 0.00.
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/lab_host="DH10B"
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/db_xref="taxon:3847"
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                                                                                                                                                                                                                               Score 56;
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
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Fax: 314 286 1810
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Seg primer: -40RP from Gibco
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/clone_lib="Gm-c1061"
/tissue_type="mature flowers of field grown plants"
/lab_host="DH108"
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                                                                                                        552 bp mRNA linear EST 19-PEB-2002 sal65g03.yl Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1061-4134 5' similar to TR:O49020 O49020 MYB-LIKE DNA-BINDING
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                                                                                 DOMAIN PROTEIN. ;, mRNA
                                                                                                                                                                 BM527774
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4353 - contact via email: ccu@resgen.com
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Fax: 314 286 1810
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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/lab_host="XL10-Gold"
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/clone_lib="Gm-c1015"
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                       TACCTCCGTCCTGATGTTAGAAGAGGGAATATTACACCCGAGGAACAACTTTTGAT 98
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae
                                                                                   soybean.
Glycine max
                                                                                                                                   EST
                                                                                                                                                                                   mRNA sequence.
BE658316
                                                                                                                                                                                                                                   BE658316 782 bg
GM700005B10E4 Gm-r1070 Glycine
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                                                                                                                                                              BE658316.1
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Fax: 314 200 2017
Email: estGen, Invitrogen Corp. 2130
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
South Memorial Parkway Huntsville, Cou@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   soybean.
Glycine max
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Location/Qualifiers
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Contact: Shoemaker R/Public Soybean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www.resgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (GibcoBrL). This library was constructed in the laboratory of Dr. Randy Sheemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="mature flowers of field grown plants"
/lab_host="DH10B"
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1061-4134"
/clone_lib="Gm-c1061"
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Pred. No.
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max cDNA clone Gm-r1070-1759 3',
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ches 0;
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REFERENCE
AUTHORS
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Other ESTs: AI930997 corresponding to Gm-c1015-278 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program
Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ystems.com web site:www.genomesystems.com
Seq primer: 5'-TTTTTTTTTTTTTTTTTTTTTTTTTTT.a'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Illinois
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213 bp mRNA

8h70908.y1 Gm-c1015 Glycine max cDNA clone

Gm-c1015-5175 5', mRNA sequence.

AW432229

AW432229.1 GI:6963536

EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="The library Gm-r1070"
/clone="The library Gm-r1070 is a sequence-driven, reracked
/note="The library Gm-r1070 is a sequence-driven, reracked
/note="The library Gm-r1070 is a sequence-driven, reracked
set of 9,216 clones selected from cDNA libraries from
set of 9,216 clones selected from cDNA libraries from
set of 9,216 clones selected from conting selected from solutions from young pods. The 5' ESTs of the source clones from
from young pods. The 5' ESTs of the source clones from
the different libraries was used to select singletons, or
a representative of each contig, which were reracked
form library Gm-r1070. The cDNA clones of the reracked
Gm-r1070 library were then sequenced at the 3' end. The
contig analysis to select unique genes was performed by
the laboratory of Ernest Retzel, Center for Computational
Genomics and Bioinformatics, University of Minnesota,
http://www.cbc.umm.edu/ResearchProjects/Soybean/index.html
Reracking was performed by Genome Systems, St. Louis,
http://www.genomesystems.com, and 3' sequencing by the
Keck Center for Comparative and Functional Genomics,
University of Illinois,
http://www.life.uiuc.edu/biotech/keck.html Note: The
corresponding 5' EST from each clone in the Gm-r1070
library is listed in the 'OTHER EST' field. The detailed
library is listed in the 'OTHER EST' for each clone can also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3847"
/clone="Gm-r1070-1759"
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545 ACAATTAATCCTGATCAATCCAGTTGTTGTACCAATGACAACAACAACA 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccueresgen.com
Seq primer: -40RP from Gibco.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                BG652172 516 bp mRNA linear EST 2: sad75b05.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEM: ID: Gm-c1051-5842 5' similar to TR:Q9SBG4 Q9SBG4 PUTATIVE TRANSCRIPTION FACTOR ;, mRNA sequence.
                                                           soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

36 g 61 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally
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/db xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-5175"
/clone_lib="Gm-c1015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="Mature flowers, field grown plants"
/lab host="XL10-Gold"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%; >--
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB Pred. No. 0.0 0; Mismatches
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RESULT 12
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                               AUTHORS
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Best Local (
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              545 ACAATTAATCCTGATCAATCCAGTTGTTGTACCAATGACAACAACAACA 593
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        Shoemaker,R., Keim,P., V.,A., Bolla,B., Marra,M.,
                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                   soybean.
Glycine max
                                                                                                                                                                                                                                              BM732162 567 bp mRNA linear EST 01-MAR-2002 sal73g09.y1 Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1061-4914 5' similar to TR:Q9SBG4 Q9SBG4 PUTATIVE TRANSCRIPTION FACTOR; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49;
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
W4444 Porest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theissing, B., Allen, M., I., Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., N., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., Public, Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 310.
Location/Qualifiers
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1 (bases 1 to 516)
                                                   (bases 1 to 567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: //note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed From floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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/lab_host="DH10B"
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Pred. No.
  Vodkin,L., Er
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0.0036;
  Erpelding,J.,
L., Kucaba,T.,
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                                                                                    Phaseoleae
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    , Khanna
Beck,C.
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Bowers
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Query Match
Best Local Similarity
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l (bases 1 to 395)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
Shoemaker,R., Keim,P., Vodkin,L., Eucha,T., Martin,J., Beck,C.,
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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Glycine max
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Gm-c1061-877
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Public Soybean EST Project
Unpublished (199)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www.resgen.com
Possible reversed clone: similarity on
Seq primer: -40RP from Gibco
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 422.
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/db xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1061-4914"
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/tissue_type="mature flowers of field grown
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gm-c1061 Glycine max cDNA clone GENOME SYSTEMS 677 5' similar to TR:Q39028 Q39028 ATMYB2. ;, mkk
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0.0033;
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                                                                                                                                                                                                                                              a; Tracheophyta;
eudicots;
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               Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., Public Soybean EST Project Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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sh58e05.yl Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE II

Gm-c1015-3993 5' similar to TR:049020 049020 MYB-LIKE DNA-BINDING
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This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
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Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW423958.1 GI:6951890
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                                                                                                                                                                                                                                                                                                             (bases 1 to 425)
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.4%; Score 47; llarity 100.0%; Pred. No. Conservative 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhOI; The CDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhOI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhOI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhOI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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/lab_host="DH10B"
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University School of Medicine
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REFERENCE
AUTHORS
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VERSION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACCTCCGTCCTGATGTTAGAAGAGGGAATATTACACCCGAGGAACA 206
                                                                                             Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Scybean EST Project Contact: Shoemaker R/Public Soybean EST Project Public Scybean EST Project
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Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Hunteville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE807621 467 bp mRNA linear EST 06-DEC-2001 ss28c05.yl Gm-c1061 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1061-33 5' similar to TR:Q39028 Q39028 ATMYB2. ;, mRNA
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Seq primer: -40RP from Gibco
High quality sequence stop: 411.
Location/Qualifiers
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EST.
                                                 Public Soybean EST Project
Washington University School of Medicine
                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Mature flowers, field grown plants"
/lab_host="XL10-Gold"
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/clone_lib="Gm-c1015"
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BASE COUNT
ORIGIN
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                                                                                                                                  Query Match 5.4%; Score 47; DB 12; Length 467; Best Local Similarity 100.0%; Pred. No. 0.012; Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1403 Std Error: 0.00
High quality sequence stop: 411.
Location/Qualifiers
1. .467
//corpanism="Glycine max"
//db_xref="taxon:3847"
//clone_lib="Gm-cl061"
//tissue_type="mature flowers of field grown plants"
//lab_host="pH109"
//lab_host="pH109"
//sisue_type="mature flowers of field grown plants"
//ab_host="pH109"
//sisue_type="mature flowers of field grown plants"
                                                                                                                                                                                                                                                                                                                   154 a
                                                                                                                                                                                                                                                                                                   /note="Westor: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Westor: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the ECORI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (GibcoBRI). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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Search completed: February 8, 2003, 11:07:15 Job time: 2058 secs

В

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgn2 1/USPTO_Spool/US10021811/runat_03022003_111222_25637/app_query.fasta_1.391
-DB=GenEmb1 -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10021811_@CGN 1 1 2425 @runat_03022003 111222_25637 -NCBU=6 -ICPU=3
-NO_XLPXY -NO_MMĀP -LĀRĞEQUERY -NEG_SCORES=0 -WAIT -LŌNGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRADS=1 -XGAPOP=10 -YGAPEXT=7
-YGAPPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                 GenEmbl: *

1: gb ba: *

2: gb htg: *

3: gb in: *

4: gb ov: *

6: gb pat: *

7: gb ph: *

9: gb pr: *

10: gb ro: *

10: gb ro: *

11: gb st: *

11: gb st: *

12: gb un: *

5: em bun: *

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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , F
2054640 seqs, 14551402878 residues
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36: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Direct Submission

Direct Submission

Submitted (05-FEB-1997) J.N. Strommer, University Of Guelph,

Submitted Noteronal Strommer, University Of Guelph,

Molecular Biology And Genetics, Guelph, Ontario NIG 2W1, CAN

Location/Qualifiers
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Y11105
T11105.1 GI:1841474
Myb-like protein; Myb26.
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Myb26: a MYB-like protein of pea flowers with affinity for promoters of phenylpropanoid genes
Plant J. 12 (6), 1273-1284 (1997)
98112025
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/protein_id="CAA71992.1"
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/db_xref="G1:1841475"
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                                                                     AL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of the clones are estimated to be 5'-truncated; less than one percent splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequences from Col-0. Genset carried out the library production and sequences from Col-0. Sequences, selection of clones, and sequence assembly.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
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2 (bases 1 to 910)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P.,
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="262460"
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                                                                           MetAspLysGlnGlnCys-----LysThrSerGlnAspProGluValArgLysGly
CGGTGGCTGAACTACCTCCGACCTGATGTGCGACGGGGAAATATCACACCAGAAGAACAG
                   2 (bases 1 to 645)
Stracke,R., Werber,M. and Weisshaar,B.
The R2R3-MYB gene family in Arabidopsis thaliana
Curr. Opin. Plant Biol. 4 (5), 447-456 (2001)
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Epermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Towards functional characterisation of the members of the R2R3-MYB gene family from Arabidopsis thaliana
Plant J. 16 (2), 263-276 (1998)
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Stracke, R. and Weisshaar
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LAKSACLKRTCKSCRLEWLNYLRPDVRRGNITPEEQLITMELLAKWGRNWSKIAKHLP
GRTDNEIKNFWRTKIQKYIIKSGETTTTVGSQSSEFINHATTSHVMNUTQETWHDWYSP
TTSYQHASNINQQLNYGNYVPEEGSIMMPLSVDQSEQNYWSVDDLWPWNIYNGN"
a 125 c 153 g 148 t
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Submitted (18-UUL-1997) Masaaki Noji, Chiba University, Facult Pharmaceutical Sciences; Yayoi-cho 1-33, Inage-ku, Chiba, Chib 263, Japan (B-mail:mnoji@p.chiba-u.ac.jp, Tel:+81-43-290-2906, Fax:+81-43-290-2905)
                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (strain:Columbia) cDNA to mRNA.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Full-length messenger RNA sequences greatly improve genome
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                          ProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLys
                                                                                                                                                                               CATGGTGAAGGTCTTTGGAACTCTGTCGCCAAAGCCTCTGGTCTAAAACGTACTGGAAAA
                                                                                                                                                                                                                   HisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLys
                                                                                                                                                                                                                                                                       GTGAGAAAAGGACCTTGGACTATGGAAGAAGATTTCATCCTCTTAATTACATCCTTAAT
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                                                                                          AGTTGTCGGCTCCGGTGGCTGAACTATCTCCGACCAGATGTGCGGCGAGGGAACATAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the creminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAer ecotypes and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="METTMKKKGRVKATITSQKEEEGTVRKGPWTMEEDFILENYILN
HGEGLWNSVAKAASGLKRTGKSCRLRWLNYLRPDVRRGNITTEEQLLIIQLHAKLGNRW
SKIAKHLPGRTDNEIKNFWRTKIQRHMKVSSENMMNHQHHCSGNSQSSGMTTQGSSGK
AIDTAESFSQAKTTTFNVVEQQSNENYMNVGDLWPVHLLNGDHHVI"
203 c 241 g 330 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="putative transcription factor"
|protein_id="AAM67076.1"
|db_xref="GI:21618026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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55.50%
51.41%
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Conservative:
Mismatches:
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Percent Similarity:
Best Local Similarity:
                                                      Pred. No.:
                                                                                                                            BASE COUNT
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                                                                     Alignment
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JOURNAL
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Isolation and characterization of the genes related biosynthesis in Asiatic hybrid lily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium; Lilium hybrid cultivars.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Faculty of Life and Environmental Sciences, Nisikawatsu 1060, Matsue, Shimane 690-8504, Japan (B-mail:nakira@life.shimane-u.ac.jp, Tel:81-852-32-6502)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submitted (24-MAR-2001) Akira Nakatsuka, Shimane University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB058642.1 GI:13537529
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                                                                                                                            269
                                                                                                                       /Godon_start=1
/protein_id="BAB40790.1"
/protein_id="BAB40790.1"
/db_xref="[gi:13537530"
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AGLKETGKSCHLRWLAYTLR PDVRRGNITPEEQLLIMELHDRWGNRWSKIAKELPGRTD
NEIKNFWRTRVQKKSKNGESSEGQISMLSDETSAMQMEDVDVGVSQTSYDQGQTSNNL
DAFEIPPEFDNILLSVESLWAMQY"
DAFFIPERGNNLLSVESLWAMQY"
a 177 c 213 g 213 t
                                                                                                                                                                                                                                                                                                                                       /cultivar="Montreux"
/db_xref="taxon:156532"
/tissue_type="tepal"
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                                                                                                                                                                                                                                                                      gene="Lhmyb"
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                                                                                                                                                                                                                                                                                                         CTGTCCGTCGAGGAACTGTGGGCTATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                        CAGACGAGCTACGATCAAGGCCAGACTTCGAACAACCTTGACGCATTTGAAATTCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerThrSerHisValSerThrMetAlaGluProMetGlu-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCATGCTTTCGGATGAAACTAGTGCCATGCAGATGGAAGATGTCGATGTTGGTGTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGACGAACAGATAACGAAATCAAGAACTTCTGGAGGACCAGAGTCCAGAAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F.CCATGGAAGAGGATCTCATCCTCATCAACTACATAGCCAACCATGGCGACGAGTCTGG
                       A family of novel myb-related genes from the resurrection plant Craterostigma plantagineum are specifically expressed in callus roots in response to ABA or desiccation Plant Mol. Biol. 32 (4), 707-716 (1996) 97134962
                                                                                                      Craterostigma plantagineum.
Craterostigma plantagineum
Eraterostigma plantagineum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiales incertae sedis;
Torentaea; Craterostigma.

1 (bases 1 to 1295)
                                                                                              Iturriaga, G., Leyns, L., Villegas, A.,
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 (bases 1 to 1295)
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myb-related transcription
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Gaps:
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n factor (cpm7)
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Direct Submission
Submitted (14-AUG-1995) Gabriel Iturriaga, Plant Molecular Biology,
Instituto de Biotecnologia, Av. Universidad #2001, Cuernavaca, MOR
                  --HisGlnAlaSerThrSerHis-
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/note="putative DNA-binding protein; Description:
gene, myb-related transcription factor"
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Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://dx.dat./cm.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin, X., Kaul, S., Town, C.D., Benito, M.-I., Creasy, T.H., Haas, B., Ronning, C.M., Koo, H., Fujii, C.Y., Utterback, T.R., Barnstead, M.I. Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M. Arabidopsis thaliana chromosome III BAC F4P13 genomic sequence unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e-mail: xlin@tigr.org
BAC clone F4P13 is from Arabidopsis chromosome III and is near the
molecular marker ILRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-JAN-2001) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Jan 24, 2001 this sequence version replaced gi:12280821.
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Submitted (16-AUG-1999) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org
3 (bases 1 to 105543)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete sequence.
                                                                        identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov). Genefinder (Phil Green, University of Washington), Genscan (Chris Burge,
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Lin, X. and Kaul, S.
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKVEPSILKEVGEPHNSSYFADQMGCDPQPQEGVGDOVTRDDETSSTAYLINKIQGKSP
LETDTQPGESHVNFGESKISSPETISSPGTHELPIADTSPLVTDNLPEKDTSETLLKS
VGRNHETHSPKSNAVELPTAHDASSQASQELQACQQDLSATSBEIQNLQQSIRSTELK
LKQSIRRDFLGTDASGRLYMGCCFPDENPRILVDGSISLQKFVQADLIGSKVPSFEL
HTVDHGRLRLSPWTYFETTEISELSELVQWLHDDDLKEEDLRESILMWKKLRYGDVQKEK
KQAQNLSAPVFATGLETKAAMSMEKRYGPCIKLBMETLKKRGKKKVAEREKLCRCEC
LESILPSMIHCLICHKTFASDDEFEDHTESKCIPYSLATEEGAGKKTKVAEREKLCRCEC
LESILPSMIHCLICHKTFASDDEFEDHTESKCIPYSLATEEGAGKKTKVAEREKLCRCEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mysrpldfrtidlrlaagaydgsteafledvlelwssirwyad
opdownyatisekfkslyraafvorlygkknyrklectsarkkkeikdivysvnkh
kapkdegrmagealesyklyrarkgrkydgeltraakeltahladvmeerdykefsae
eriillkkilodellssslvhohleocaeaiiemooklrsissekknakkroefltakl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLNYKSSAGKDVABISNYSBLDSGLIRYQEBESISPYHFEBICSKFVTKDCNRDLVKB
IGLISSNGIPTFLPSSSTHLNDSVLISAKSNKPDGGDSGDQVIFAGPETNYEGLNSES
NMSFDRSVTDSHGGPLDKPSGLGFGFSEQKNKKSSGSGLKSCCVVPQAALKRVTGKAL
                                                                                                                                                                                                                                                        /note="exon predicted by marginal shadowexon"
                                                                                                                                                                                                                                                                                                                                                                 DSCDSYFPSIVPIQDNSNASDHDNDRSCFADVFVPTTSDSHDHHGESLAFWGWP"
complement (6749. .6849)
                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mesnsffddbashgnsmfflgnlnpvvQgggarsmmneetsk
Rraffsspedlydddfydddlekkkrlttegyhlleksfettentgleberktglekstyst
Teklqgkqetaneppgqvbepnqldpvytinaaaiktedrlssgsvgsavldddapqll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="homeobox-leucine zipper protein HAT5 (HD-ZIP protein 5) (HD-ZIP protein ATHB-1)"
/protein_id="AAF01532.1"
/db_xref="GI:6016706"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="exon predicted by xgrail, quality good"
complement(4496. .6383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLPDQKSQPVSDSQERSSRVRRSGKKRKEPEGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGFRFLKTNLLDMDVÅLPEBÅLRPSKSHÞNRRRÅWRVFVKSSQSIYELVQATIVVEDM
IKTEYLKNEWWYWSSLSAAAKISTLSALSVRIFSLDAAIIYDKPITPSNPIDETKPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F4P13.1"
join(<47. .145,499.
3721. .>4029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                complement(8901. .8985)
/note="exon predicted by
marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (join (4639. .4989,5292. .5531,5619. .5758,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F4P13.1"
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/chromosome="III"
                                                                           marginal
                                                                                                                                                                                                                                                                                                                                   /note="exon predicted by xgrail, quality marginal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5938. .6025))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (join (4496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="identical to home
(HD-ZIP protein 5) (HD-)
[Arabidopsis thaliana]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F4P13.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db xref="GI:6016705"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="F4P13.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721. .4029)
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                                                                                                                                                                                                          /note="exon predicted by
                                                                                                                                                                                                                                          complement (6934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F4P13.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F4P13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAF01531.1"
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     [ement (9068
        family="(GAAAA)n"
[ement(9068. .9130)
                                                                                                                                                         family="(TAAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6383
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2
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5) (HD-ZIP protein ATHB-1) G
                                                                                                                                                                                                                                             .6974)
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                                                                                                                                                                                                             quality good"
                                                                                                                                                                                                                                                                                        quality
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GB:Q02283
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                            complement (15294...15377)
/rpt_family="POLY A"
complement (1606...16141)
/note="exon predicted by xgrail, q
complement (16294...16416)
/note="exon predicted by xgrail, q
complement (16681...16714)
/rpt_family="POLY_A"
                                                                                                                                                                                                                                                                                   /rpt family="(CAA)n"
complement (15273. . 15370)
/rpt family=""(TAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="F4P13.3"
join(10560. .107
12047. .12189 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to ATMRK1, an Arabidopsis protein kinase related to mammal mixed-lineage kinases and Raf protein kinases BLBAA22079 (Arabidopsis thaliana]" complement (join(<13086. .13292,13396. .13705,13791. .13987, 14252. .14373,14850. .>15249))
/gene="FP471.4" complement (join(13086. .13292,13396. .13705,13791. .13987, 14252. .14373,14850. .15249))
                                                                                                                                                                                                                                                                                                                                                               / tränelation="MKEKAESGGGVGYVRADQIDLKSLDEQLQRHLSKAWTMEKRKSI
SDGEDNVNNTRHNQNNFGHPQLVFQRFLLGGGYSNNNNSSKNDI ITSTEVEKSSREEG
IDESKLIIKSVLARGTFGTVHRGIYDGQDVAVKLLDWGEEGHRSDAEIASLRAAFTQE
VAVMHKLDHENVTKFIGAAMGTSEMSIQTENGQMGMPSNVCCVVVEYCPGGALKSFLI
KTRRKLAFKVVIQLSLDLARGLSYLHSQKIVHRDVKTENMLLDKSRTILKIADFGVAR
LDASNENDMTGGTGTLGYMAEBVLNGSEPNIKCDVYSFGICLMEIYCCMPYPPDLSFS
EVTSANVRQNLRPEIPRCCESSLANVMKRCWDANPEKRPEMEEVVAMLEAIDTSKGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /genc="F4P13.4"
/codon_start=1
/codon_start=1
/product="putative protein kinase"
/protein_id="AAF01534.1"
/db_xref="G1:6016708"
/db_xref="G1:6016708"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tranalation="MAAAPASLPTFSVVNSSRPPRRRIGFSCSKKPLEVRCSSGNTRY
TKQGGAFTSLKECAISLALSVGLMVSVDSIALPRAHAVANPTDVSVTLISGPPIKD
PEALLRYALPIDNKAILEVQKPLDSITDSLKTLAGVKALDSVBRNVRDASTLOQKSLI
TVAGFBAESKKDHGNEMIEKLEAGMQDMLKIVEDRKRDAVAPKQKEILKYVGGIEEDMV
IVAGFBAESKKDHGNEMIEKLEAGMQDMLKIVEDRKRDAVAPKQKEILKYVGGIEEDMV
DGFPYEVPEEYRMMPLLKGRASVDMKVKIKDNENIEDCVFRIVLDGYVAAPVTAGNFVD
LVERHFYDGMEIQRSDDGFVOOTGDFBGABASTDDSTEKTRTVPLEIMVTGEKTPFVG
STLEELGLYKAQVVIPPNAFGTMAMAREEFENDSGSSQVFMLLKESELTPSNSNILDG
RYAVFSVTDNEDFLADLKVGDVIESIQVVSGLENLANPSYKIAG"
COMPLEMENT (12357. 12380)
// Tyt. family=" (GAA) n" 15340."
                                                                                                                                                                                                                                                                                                                                                   MIPPDQQQGCFCFRRHRGP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="exon predicted by xgrail, quality complement (10351. 10380) /note="exon predicted by xgrail, quality marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (<13086. .>15249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(10560. .10700,10996. .11289,11419. .1
12047. .12189,12276. .12347,12438. .12665)
/gene="F4P13.3"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative thylakoid lumen rotamase"
/protein_id="AAF01533.1"
/db_xref="GI:6016707"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to thylakoid lumen rotamase GB:CAA72792
(Spinacia oleracea)"
|oin(10393...10700,10996. .11289,11419. .11618,11732.
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     2.1e-42
519.50
51.08%
43.88%
45.65%
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family="(TAAAA)n"
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.12189,12276. .12347,12438. .12821)
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         Length:
Matches:
Conservative:
Mismatches:
Indels:
       105543
122
20
24
93
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                                                                        SOURCE
ORGANISM
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ACCESSION
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US-10-021-811-36 (1-206) x ATAC009325 (1-105543)
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                                                                                                                                                                                                                                                                                                                                                                                                                      GAGAATTACTGGAACGTTGAAGATCTGTGGCCCCGTCCACTTGCTTAATGGTGAC 32358
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTCAGAGACACATGAAAGTGTCATCGGAAAATATGATGAATCATCAACATCATTGTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGACGTTTAATGTGGTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaGluProMetGluMetTyrSerProProCysTyrGlnGlyMetLeuGluProPheSer 168
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Oryza sativa (japonica cultivar-group).
Dryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1343)
                                                                                                                                                                                                                                                             AY026332 1343 by Oryza sativa Myb transcription
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                                                                                        AGAGTGCAAAAGCATGCCAAGCAACTCAATTGTGATGTCAACAGCAAGAGGTTCAAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1343)
Lee,M.-W. and Yang,Y.
Direct Submission
Submitted (29-JAN-2001) Plant Pathology, U
217 Plant Science Bldg., Fayetteville, AR
Location/Qualifiers
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wel jasmonic acid-inducible rice myb gene associates with
vel jasmonic acid-inducible death
al infection and host cell death
plant Microbe Interact. 14 (4), 527-535 (2001)
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/product="Myb transcription factor JAMyb"
/proteain_ide"AAK08983.1"
/broteain_ide"AAK08983.1"
/db_xref="GI:13177578"
/translation="MEMYLORTSHHPVDGEQQEAAAELSSAELRRGPWTVDEDLTLIN
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YISDHGERWNALARTDMSIKNYWRTRVQKHAKQLNCDVNSKRFKDAMKYLWMPRLAER
GNRWSKIAGHLFGRTDMSIKNYWRTRVQKHAKQLNCDVNSKRFKDAMKYLWMPRLAER
IHARAGAVDDSGDYSNNDLSCVSGVTWATVANCEDGSSSMVTSSSSDSTTSESQDLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="related to host cell death and defense responses;
induced by jasmonic acid, wounding, or infection of rice
blast fungus, but not by salicylic acid or abscisic acid
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/cultivar="Drew"
/db_xref="taxon:39947"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiales incertae sedis;
Torenieae; Craterostigma.
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Villalobos,M.A., Bartels,D. and Iturriaga,G.
The Craterostigma plantagineum CpMYB10 gene
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Villalobos, M.A. and Iturriaga,
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                                                                                                                  AQENSSTVASSESFGSLSSELTAEANYANYHRVINGADHQQIDSSTTSYDWQNCAVGN
NGNSDQLGMGFADDRRSNEQWMMMTDDVVDNGGSSDQDNNLWNVDDVWFLQQFSSCF"
1 265 c 271 g 252 t
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AHHGEGRMNSLARFAGLKRTGKSCRLARVLNTARPVERGNITLEEQLLILELHSRWGN
RWSKLAQHLGRGTDNEIKNYWRTRYQKHAKQLKCDVNSKQFKDTMRYLWMPRLIVERIG
ASATTDDGAPPAVASSPSSAMNTACYSAAMAAGDHRRQFMLMPQYXATTTTTHNNSMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                 /codon_start=1
/product="MYB transcription factor"
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/db_xref="GI:21215202"
                                                                                                                                                                                                                                                                                                    gene="MYB10"
                                                                                                                                                                                                                                                                                                                     79. .1080
                                                                                                                                                                                                                                                                                                                                   'note="CpMYB10"
                                                                                                                                                                                                                                                                                                                                                  'gene="MYB10"
                                                                                                                                                                                                                                                                                                                                                                                     'organism="Craterostigma
'db_xref="taxon:4153"
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Percent Similarity: Best Local Similarity:

following:

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AP003140
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProPheSerThrGlnPheProThrIleAsnProAspGlnSerSerCysCysThrAsnAsp 185
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                                                                                                                                    Oryza sativa nipponbare(GA3) genomic DNA, clone: OSJNBa0025P13
Published ~~ 1
                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Submitted (31-JAN-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kann
                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
BAC clone:OSJNBa0025P13.
AP003140.
AP003140.2 GI:14164491
                                                                                                                                                                                                                                                  Spermatophyta;
Ehrhartoideae;
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                                                                           Yamamoto, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTR2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from -21M1 to M13rev of the BAC clone. This sequence of OSJNBB0025P13 clone has an overlap with P0702D12 (DDBJ: AP002882) clone at the position 1 to 1534 of 5' end and with P0487H02 (DDBJ: AP002883) at the position 84175 to 133242 of 3' end. The sequence of this clone starts at the position 135799 of P0702D12 and ends at the position 49068 of P0487H02. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp), URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7461)
Tel:81-298-38-7441, Fax:81-298-38-7468)
On May 21, 2001 this sequence version replaced gi:12641874.
Genes were predicted from the integrated results of the following GENSCANI.0, BLASTNZ.0, BLASTNZ.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr
                               /product="putative shaggy-related protein kinase"
/product="putative shaggy-related protein kinase"
/protein id="BAB55743.1"
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YNKMSQRMPLLYVKLYWYQICRALAYIHNCYGVCHRDIKGONILVNPHMDLKLCDFGG
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SGVDQLVEIIKVLGTPTREEKHMENNYTEFKFFQLIKAHPMHKIFHKRMFSEAVDLVS
SGVDQLVEIIKVLGTPTREEKHMENNYTEFKFFQLIKAHPMHKIFHKMFSEAVDLVS
                                                                                                                                                                                                                                                                            CPSKKSTPMKDLLDTRLPPDAEVIALKIW"

join(9270. 9380,9468. 9560,9738. 9797,9871. 10143,
10245. 10319,10435. 10491,10609. 10749,10829. 10879,
10972. 11067,11175. 11258,11346. 11448,11534. 11616)
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join(9270. 9380,9468. 9560,9738. 9797,9871. 10143,
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10972. 11067,11175. 11228,11346. 11448,11534. 11616)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative protein kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .133242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5040,5244.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MDVVNIGRKTNKQTANQPKKANAMHSQIDTTSSIGNFIDIDKKK DNLNYESYTIVAHTEYYRSIYANLIRLAAIK" complement (join(31012. .31020,31243. .31294,31358. .31478, 32907. .33108,34245. .34337)) /gene=OSJNBA0025913.6"
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GISIGSLGKAGTKACVANVTVRNAVIRHSDNGVRIKTWQGGSGSVSAVAFENVRNDAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAAHPPSQAPGPAARHAPGPARHHGAPAPHPGRRSPPAPANPPSSDPMPGGAPSAA
PAAGAATVYDI VKDFCAAGDGVTDJTDALKTAMDTACADDGAGVTLAAAGRSFLLHTT
VFTCBCQGSVTLQUDGTI VAPSEPATWPANNKERMILVFYRADGVSLVGAGALIDGKGGV
WWDLPCKPHKGGNTHGPCDSPVAMRFAI SNNVTVRGLKVQNSPEFHFRFDNCNGVRVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(31012. .31020,31243. .31294,31358. .31478, 32907. .33108,34245. .34337))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="OSJNBa0025P13.5"
complement(join(27109. .27305,28392. .28419))
/gene="OSJNBa0025P13.5"
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/gene="OSJNBA0025P13.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSDVELLPASGDTVDEPFCWNVYGNAATFTVPPVSCLSSGFPNYTEKKDLQCY"
complement (join (21118. . 22066, 22246. . 22397, 23530. . 23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(15137. .15820,15928. .15963,16058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join (27109. .27305, 28392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHHQLLPPPHTDPPPAAFPPDPATAARI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAAI SNPAADAPSKRSSMPPARTPSLS PSPPPPPPSS PSSAPATTNCRRHPTTFHPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCKPPAPPTQPPQRRRRALRCRRDHHRGKTISSAWIRSPMPASPLDPASVANLTATSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative polygalacturonase-like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="OSJNBa0025P13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSVATSCSDCRAYIPSVVWNVILPIQLSSGMEDRLVCTPLFVPICFGKQKVPPNVW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="OSJNBa0025P13.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MELAAAGRTAAIALLLALAFASSFISAADGARSARHHHAKHAKR/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="OSJNBa0025P13.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="hypothetical protein"
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QVERANAEILKGLKTKTFNILKKHGDSWIEKLPAVLWANRTTPSRATGETSFFLVYGA
EAVLPSELTLRSPRVTMYCEADQDQLRRDDLDYLEERRRRAALRAARYQQSLRRYHQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMQFDGSLSLQGAGAGVTLTSPSGDVLRYLVRLDFRATNNMAEYEGLLAGLRVAAGLG
IRRLLVLGDSQLVVNQVYKEYRCSDPQMDAYVRQVRRMERHFDGIELRHVPRRDNAVA
DELSRLASSRAQTPPGAFEERLAQPSARPDPLGETDAPERPPRPIGVQASGPEGSAPS
PRDGGPGGSRPADARGKRKQEGTPPPSPPRGGGAVRASSRRPEGAVPTPQPEGERKKK
RLRKMGGIVPCRGNLSLQGVTEPHLAPKRDPVAPPLPPPPPRHSKSGRSEAEETVTAE
                                                                             LCEMFIRVRESLRLFRWFFTVQPVSPPTAVGGCYFQPRGQYLARYIPCVLRKKMDDWK
SDWFYTPLGEBARLRLPSQPPAQASSWRATVDLGDGYDAVLDRLAGLRSQGLTGAMVF
GDYLRRRIAFLQRRAAGAWBYTGFBDYMRTHJGGKKMUMDFBDFSMVVQRYLNLISSVEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar to Oryza sativa chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="OSJNBa0025P13.8" complement (join (45140. .45474,45602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47154. .48413)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join (45140. .45474, 45602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNIEHLRRFYP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVRARSLCVDDLVLRRVQTRAGLSKLSPMWEGPYRVIGVPRPGSVRLATGDGTELPNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKHSALKFIRGITARFGVPNRIITNNGTQFTSELFGDYCKDMGIKLCFASPAHPRSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTHQPAQALQTIPLSWPFAVWGLDILGPFRRAPGGFEYQYVAVDKFTKWPEAYPVIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPRLIAWTTEIQTYLADKTLPEDREGSERVRRISKRYVLVEGTLYRRAANGVLLKCIP
REQGVELLADVHEGECGAHSASRTLVGKAFRQGFYWPTALNDAVDLVRRCRACQFHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVRWAIELSEFDLRFEPRHAIKSQALTDFVAEWTPAPEPVSAPEASSGTSQLPHTAYW
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                      AsnTyrIleAlaAsnHisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                        SerGlnAspProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMet
-----HisGlnAlaSerThrSerHisValSerThrMetAlaGluProMetGluMetTyr 155
                                               GTCAATAGCCGCCAGTTCAAGGACGTCATGAGGCACCTCTGGATGCCGCGCCTCGTCGAG 120532
                                                                           SerAsnAsnSerGluIleAsnAsp------
                                                                                                                                  TyrTrpArgThrArgIleGlnLysHisIleLysGlnAlaGluAsnPheGlnGlnGlnSer 129
                                                                                                                                                                AACCGCTGGTCCAGGATCGCGCAGCACATGCCGGGGAGGACGACAACGAGATCAAGAAC 120424
                                                                                                                                                                                AsnArgTrpSerLysIleAlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsn 109
                                                                                                                                                                                                                           CGCGGCGACTTCACCCCGCAGGAGCAGCTGCTCATCCTCGAGCTCCACTTCCGGTGGGGG 120364
                                                                                                                                                                                                                                           ArgGlyAsnIleThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTrpGly 89
                                                                                                                                                                                                                                                                                     AGGCGCACGGGAAGAGCTGCCGCCTCCGGTGGCTCAACTACCTCCGCCCCGACGTGCGC 120304
                                                                                                                                                                                                                                                                                                                                               GCGGAGGAGGAGGATGTTCGGAGAGGGCCGTGGACGGTGGAGGAGGACGCGGTGCTGGCC 120184
                                                                                                         DAGGGTGCAGAAGCACGCCAAGCAGCTC-------GGCTGCGAC 120472
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514.50
56.50%
45.12%
45.21%
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Matches:
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
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111
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40
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	FEATURES Location/Qualifiers
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/product="putative MtN21" /protein id="BAB67846.1"	Detailed information on overlap and assembly quality together with
<pre>/note="contains EST C99297(E10619)" /codon_start=1</pre>	This sequence of P0487H02 clone has an overlap with P0682B08 (DDBJ:
/gene="P0487H02.5"	
7H02.5"	almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program one
AAT"	-
GTAGGCVSQRGTNSGDGVGRGARRLGRRRQMLRLSRGVCHCDAAACATRGNNARPMMP CGGCDAGGTSAVVPTHPRRFRWRWSIVPTPSNLINKTGSSSSYHCKKIGKEKRETITD	A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level
/translation="mrthtrtggrahpagspycDthaDaaqsymLwekLarDraypng ATRISPERNIKYRPRLRLICHRGAPTTGGRQRQORLEAWPAGGDRPYRCPRHGEARRR	corresponding DDBJ accession no. and RGP clone ID.
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/yene="roto/nuz.t" /note="hypothetical protein"	NCBI NonRedundant Protein database, nr
complement (join (1018110287,1133811896))	GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against
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ADMVGETNKEPPAQSGKKKGVVLISKFICIIRQTEYLSLSPLDPSSPYQIISRVN"	. U (
/db_xref="GI:15623784"	(E-mail:tsasaki@nias.affrc.go.ip.UR:http://rm.dna.affrc.go.ip/
/cocon start=1 /protein id="BAB67844.1"	Agrobiological Sciences, Rice Genome Research P.
/note="hypothetical protein"	JOURNAL Submitted (11-0CT-2000) Takuji Sagaki. National Tretitite of
JOIN(8658: .8923,8973: .9006) /gene="P0487H02.3"	AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
/gene="P0487H02.3"	
join(86588923,89739006)	clone:P0487H02
/translation="MNRPSTINVLIVHEVQKFLVHTNFSSCRENNEPRKISPRIQSAA	AUTHURS Sasaki, T., Matsumoto, T. and Yamamoto, K. TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
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/gene="P0487H02.2" /note="hypothetical protein"	Eukaryota; Viridiplantae; Streptophyta;
join (7576 7805, 8020 8053)	;
Join(75767805,80208053) /gene="P0487H02.2"	SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
PPYLCSDNGKWSRAPTDPQGQVERCFPERGPSIHSPPVWILP"	APUUZBB3.2 GIIL5623/BI
FEYYWSELDELDGRMLFYGLGCSRSYKAGDGRYPGMEEGVYFLDDPSIHQMIIGDAPK	ON AP002883
DNP1MRLEEVEDLLCHHGAFHFLTRAEDVLACEEPPVFYRDSVSLVPANMFFLPRVHD ENETVLARYLMSGCKKLLMVVDLASGCGCGDTTGAEGVFGKKKENTGEEDEGGAGGAGGAG	PAC clone:P0487H02.
MAIVAATUSCOPTEQGCIVAGIIESSPNLVAVGHVTRSIAFWRMGDQVVLPVLWALEE	883 145491 bp DNA linear PLN 21-MAR-
RHMGRVCNSWRVALVKLKAPAPPPPLPWLALPESDDGLPATVSCVLSGCRTHAFSVLQ GARGAPVFGSVNGGWLFLAVGGCAACCOALL NI X INGECTLAIL AND ANNOVADARD DE	AP002883
AADQERERPPRSEESLTTPRSIPSLIPSMADQLRRRWAAADDGVLYEVARRIPCEIDR	3
GEAGGGGNDTGRAAAAAPLPLPPSQIWPEEGGGRLAAVATAWSGDVVPHWHETPSTSD	Db 120812 7FC64664676767 120829
HKCKRPSAANARPNRDARRGRTIPRRLDRDQITRPASQRKGLCTGTPCLRMSSQNHTI ITSYDYYVVIIVITCGLIRPVFGSLSHPCSDLARGGRGRAGGDGNGVEWWOHLAGGGR	Qy 194 MetGluAspSerTrpSer 199
/translation="MQSRGHGRSTRGTSQGLARCSVSKDEKYLCVNGSNCMPHPQTTT	Db 120752 AGCGAGCAATGCGGCAGCGCCACCACCAGCGTTGGGATCAGTTATGACATG 120811
	QY 180
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.5186,5198	
complement (join 61328, 20162113, 21492286, 25212676,	
.5186,5198	Db 120632 TCAACCACGACGTCGAGCATGGCAGGGTCGCTGACGCACGGCGAGGAGTTCCCGTTGC 120691
	Qy 167 PheSerThr
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	Qy 156 SerProProCysTyrGlnGlyMetLeuGluPro 166
1145491	pp 120533 AGGATCCACGCCGCCGCCTCGTCGGAACGCGCCGCCGC 120574 source

gene

SdC

CDS gene gene

Sg

145491 111 28 40 67

.43552)) .43552))

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CALSNTLPALTFAMAAAFRMESVRLSAAAGQAKVFGTVVCVGGSMIMPFYKGPLLRLW
ASPIHMRFAESAASGAAAPAAGGAAVLGDVLIILSCAAMAVMFITIQTKWSERFSAPYT
STTIMCLMAGVQCAGVSAAMDRSVAWKLGFDIILSVSVLYIGVVGSGIAFALMSWCIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mpgaswiltaachggtdsanggocrvswtrvcrprdlgglgipd lrvagfalrvrwlmlorsghpywsdlkasversvsdmfaastfsilgdgostlfwtdr widgrsiasiafdllhvvprrfgosrtvaaglangwydicaltvpvisgfllwtdr AvpetolspecedhlvwrwtgdocysaosayQafflogwsfacadllwakgbakkyr flwfaffortwfadlcysaosayQafflogwsfacadllwakgbakkyr flwfaffortwfadllokgrgidshsacpfcaqeletanhillidcvfarqvwlpgsrig ghplgyvylstfaaastpwys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join (21707. .21839, 22076. /gene="P0487H02.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (join (30213. .30418,31118. .31292,32407)
33634. .33894,33932. .34047,34149. .34246,34509.
/gene="P0467H02.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(27604. .27686,27736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (join (27604. .27686, 27736. /gene="P0487H02.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (join (21707. .21839, 22076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join (30213. .30418,3111 ) 33634. .33894,33932. .34047,34149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein similar to Oryza sativa chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIGNNVVMDDEW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB67848.1"
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RDDLQXMNEIVAGNEMQRLGLWKSFTSLHQLALECGVKSSIPAHPDETSEPKLGRVQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join (23501. .23554, 23930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join (23501. .23554, 23930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0487H02.6"
                                                                                                                                                                                                                                                                                NRPAAAPPHRPIGARRLLLSVAAHHAHRLVSLV" 35906. .36787
                                                                                                                                                                                                                                                                                                                                             GKTGKMLYSHEEDIRLEEQHKATTELDLHELGVVVHGFGRIGGAVEWKDATTTDGREA
RREAGSKDNFQRGDGIGDGVCGGPIPYPCFGRIRSGSDRILSDPFSPLESIYYILKVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB67849.1"
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                                                                                                                                                                                                                                     /gene="P0487H02.10"
35906. .36787
                                                                                                                                                                                                                                                                                                                           FKLPTNALMPPHRIPINAPKPRRALLSRAVELSALGVSRDGVTSQLRKPLRDCVVVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/db_xref="GI:15623790"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="hypothetical protein"
                                                                                                                                                                                          /gene="P0487H02.10"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon
                                                                                                         /protein_id="BAB67851.1"
/db_xref="GI:15623791"
                                                                                                                                                                    product="putative dehydration-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="P0487H02.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .34246,34509.
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                                                                                                                                                                        myb-related
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.34561))
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnTyrIleAlaAsnHisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerGlnAspProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scores:
                                                                                                                                  TTCGAGGGGAGCTGGTCG 36655
                                                                                                                                                                           MetGluAspSerTrpSer
                                                                                                                                                                                                                                                                                                         TCGACGAACCACCTGATGACCATGGCCAGCGTCACCACCGCAGCGGCAGATTGGTCC
                                                                                                                                                                                                                                                                                                                                                                                          TCAACCACGACGTCGAGCATGGCAGGGTCGTCGGTGACGCACGGCGAGCAGTTCCCCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                       PheSerThr----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerProProCys-----GluPro 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGATCCACGCCGCCGCCTCG-----TCGGAACGCGCCGCCGCCG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HisGlnAlaSerThrSerHisValSerThrMetAlaGluProMetGluMetTyr 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCAATAGCCGCCAGTTCAAGGACGTCATGAGGCACCTCTGGATGCCGCGCCTCGTCGAG 36358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerAsnAsnSerGluIleAsnAsp-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrTrpArgThrArgIleGlnLysHisIleLysGlnAlaGluAsnPheGlnGlnGlnSer 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCGCCACTTCACCCCGCAGGAGCAGCTGCTCATCCTCGAGCTCCACTTCCGGTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgGlyAsnIleThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTrpGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCGCACGGGGAAGAGCTGCCGCCTCCGGTGGCTCAACTACCTCCGCCCCGACGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuArgProAspValArg
                                                                                                                                                                                                                     AGCGAGCAATGCGGCAGCGGCAGCGCCACCAGCACGAGCGTTGGGGATCAGTTATGACATG 36637
                                                                                                                                                                                                                                                                Ser---
  AF262733 1423 l
Arabidopsis thaliana putative
mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - CCGCCGTGTGCCGCCGCCGGCTAGTCACAGCGGCATGTGCCCACTCACCTGACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(41992. .42118,43485.
/gene="P0487H02.11"
complement(join(41992. .42118,43485.
/gene="P0487H02.11"
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514.50
56.50%
45.12%
45.21%
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Matches:
Conservative:
Mismatches:
Indels:
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                                               å
                             bp mRNA
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------GGCTGCGAC 36298

109

36190

36250

89

69

36070

36130

49

36010 29

137

GlnPhePro--- 172

36457

36400

36517

36577

gene

CDS

gene

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linear PLN 30-AUG-2001 1 factor MYB108 (MYB108)

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                                        AITGGATGAAAAAGGAAGAAGCTTGAAGAACAACAACATGGAAGACGAGATGGACCTAAAG
LysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHisGly 36
                                                                               MetAspLysLysGlnGlnCysLysThrSerGlnAspProGlu------valArg
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On Aug 30, 2001 this sequence version replaced gi:8101955
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Submitted (02-MAY-2000) Biochemie, Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln D-50829, Germany
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The R2R3-MYB gene family in Arabidopsis thaliana
Curr. Opin. Plant Biol. 4 (5), 447-456 (2001)
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/protein_id="AAF72668.1"
/db_xref="GI:8101956"
/translation="MODEKGRSLKUNNNEDDEMDLKRGDWTAEEDFKLMNYIATNGEGRW
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LPGRTDNEIKNYWRTRYOKHAKQLKCDVNSQOFKDTMKYLWWFRLVERIQSASASSAA
AATTTTTTGSAGTSSCITTSNNQFMNYDDYNNNNMGQOFGWMSNNDYITPENSSVAV
SPASDLTEYYSAPNPNPEYYSGOMGNSYYPDGNIVSSQLLPDNFDYSGLLDEDLTAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="At3g06490; member of the R2R3-MYB family"
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db_xref="taxon:3702"
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E 2 (bases 1 to 1140)

Stracke,R. and Weisshaar,B.

Direct Submission

L Submitted (10-JAN-2001) Dept. Plant Breeding and Yield Physiology,
Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg

10, Koeln D-50829, Germany

3 (bases 1 to 1140)

Stracke,R. and Weisshaar,B.

Direct Submission

L Submitted (29-AUG-2001) Dept. Plant Breeding and Yield Physiology,
Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg

10, Koeln D-50829, Germany

C Sequence update by submitter

On Aug 30, 2001 this sequence version replaced gi:13430155.
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Stracke,R., Werber,M. and Weisshaar,B.
The R2R3-MYB gene family in Arabidopsis thaliana
Curr. Opin. Plant Biol. 4 (5), 447-456 (2001)
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 GlnSerSerCysCysThrAsnAspAsnAsnIleAsnTyrTrpSerMetGluAspSer
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                                                                                                                                                                                                                                                                                                                                     TACCTTAAACCCGACATAAAGGGTGGGAATCTCACTCCTCAAGAACAACTTTTAATCCTT
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                                                            MetLeuGluProPheSerThrGlnPheProThrIleAsn----
                                                                                                                      SerHisValSerThrMetAlaGluProMetGluMetTyrSerProProCysTyrGlnGly 162
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ANAPDLIGPILRDSKNIGFNNNDCSTSNSEDLKKTSOFMDFSDLETTWSLEGSRGGSS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-AUG-2001) Dept. Plant Breeding and Yield Phys Max-Planck-Institut fuer Euchtungsforschung, Carl-von-Lin 10, Koeln D-50829, Germany Sequence update by submitter on Aug 30, 2001 this sequence version replaced gi:11641119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 931)
Stracke,R., Werber,M. and Weisshaar,B.
The R2R3-WYB gene family in Arabidopsis thaliana
Curr. Opin. Plant Biol. 4 (5), 447-456 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                          note="ecotype:
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                        630 ÁGCGTCGCCÁCC 641
           180 SerCysCysThr 183
                                                            142 ThrSerHisValSerThrMetAlaGluProMetGluMetTyrSerProProCysTyrGln 161
                                                                          495 -----CTTCTAAAATGTGACGTGAACAGCAAGCAATTCAAAGAC------ACC 536
                                                                                                   102 ArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGlnLysHisIleLysGln 121
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                                                                                  122 AlaGluAsnPheGlnGlnGerSerAsnAsnSerGluIleAsnAspHisGlnAlaSer 141
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Search completed: February 8, 2003, 11:57:47 Job time: 2716 secs

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-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR_MIN=0 -ALIGN=15
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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N Geneseq 101002:*

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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution. printed,

## Result No. 539 523.5 510 495 478 478 667 625.5 402.5 402.5 402.5 400.5 397.5 396.5 396.5 396.5 396.5 396.5 396.5 396.5 396.5 396.5 396.5 396.5 396.5 396.5 421 410.5 410.5 406.5 406.5 405.5 384 383.5 383.5 383 Score Query Match 59.0 58.6 55.0 51.4 51.4 47.5 47.5 Length 1137 981 972 626 526 539 959 389 417 516 660 542 389 1081 1820 1082 1774 1218 1209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 11209 1 1127 673 DB ij AAC42228 ABK65183 AAC56434 AAC56837 AAF90596 AAC44207 AAT60745 AAC43611 AAD06456 AAC57245 AAD05764 AAF90594 AAT60744 AAC57346 ABK65317 ABK65247 AAZ46048 AAH28336 AAC42662 AAD05748 ABK65181 AAD05784 ABK65252 ABK65364 AAH87724 AAC57194 AAC5572 AAC44894 AAC56152 AAC56774 AAC56774 AAC56352 AAC41714 AAC37953 AAC56197 AAF85188 AAX25571 AAC57337 AAC40587 AAC57336 ABK65248 SUMMARIES

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## 25-JAN-2001 AAC57336; AAC57336 standard; DNA; (first entry) 862 BP

ALIGNMENTS

Eucalyptus

grandis transcription factor DNA sequence #773.

RESULT 1
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XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 CysZHis2; CCAAT box element; MYB; ss. Eucalyptus grandis

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and ERBBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements and wron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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{\tt I...eLysGlnAlaGluAsnPheGlnGlnGlnSerSerAsnAsnSerGluIleAsnAspHis}
                         LeuProGlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGlnLysHis
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                                                  Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                          Arabidopsis thaliana.
                                                                                                                      Arabidopsis thaliana DNA fragment SEQ
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ATGGAGAAAAGGAGAAAGTAGTGGTGGGTCTGGATCAGGAGATGCAGAGGTGAGAAAAAGGG
  LeuProGlyArgThrAspAsnGluIleLysAsnTyrTzpArgThrArgIleGlnLysHis
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  The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, LIM domain, AP2
                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynuclectide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                         Claim l; Pages 649-650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGACGTTTAATGTGGTG---
                                                                                                                                                                                       GCTGAGAGCTTCTCT---
                                                                                                                                                                                                                               GGAAACTCACAGAGCTCGGGGATGACGACGCAAGGCAGCTCCGGCAAAGCCATAGACACG
                                                                                                                                                                                                                                                    AsnAsnSerGluIleAsn-----AspHisGlnAlaSerThrSerHisValSerThrMet
                                                                                                                                                                                                                                                                                                                                                                                    ProGluGluGlnLeuIleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                            SerCysArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetAspLγsLγsGlnGlnCysLγs-----ThrSerGlnAspProGlu-----
                                                                                                                                                                                                                                                                            ATTCAGAGACACATGAAAGTGTCATCGGAAAATATGATGAATCATCAACATCATTGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                              AGTTGTCGGCTCCGGTGGCTGAACTATCTCCGACCAGATGTGCGGCGAGGGAACATAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGAAAAGGACCTTGGACTATGGAAGAAGATTTCATCCTCTTTAATTACATCCTTAAT
                                                   standard;
       (first
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99US-0161406.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161993.
99US-0161993.
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585.00
65.14%
55.50%
51.41%
                                                   DNA;
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Conservative:
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Gaps:
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                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EEBBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
                                                                                                                                                                                                                                                                                                                                     Sequence 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 131; 747pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-579369/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant; transcription factor; gene expression; eucalyptus; pine; poplar; sweetgum; teak; mahogany; bZF; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-)
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                                                                     57
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                    77
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                                                                                                                                              GluGlnLeuLeuIleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLysIleAla
                                                         ArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGlu
                                                                                                             GluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCys
                                                                                                                                                                                                                                                                                                             Scores:
                                                                                             GAAGGACGCTGGAACTCCCTCGCCCGCAGCGCAGGTTTGAAAACGGACCGGAAAAGAGTTGC
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FLETCHER CHALLENGE FORESTS
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                                                                                                                                                                                                                                                                                                                                     BP;
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99US-0149485.
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540.00
61.99%
51.13%
47.45%
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Mismatches:
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RESULT
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17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                       Transcription factor; biochemical characteristic; controlling structural characteristic; developmental characteristic; gene agricultural biotechnology; plant trait modification; ss.
                                                                                                                                                                                                                                                                                                                                                                                 AAD05784;
                                                                                                                                                                                                                                                                                                                                                                                                     AAD05784 standard; cDNA; 1137
                                            (MEND-)
(CREE/)
(YUGG/)
(ADAM/)
                                                                                                                                            14-NOV-2000;
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                                                                                                                                                                                                                                                                   Arabidopsis
                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana transcription factor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysHisIleLysGlnAlaGluAsnPheGlnGlnGlnSerSerAsnAsnSerGluIleAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGln
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ADAM L.
RIECHMANN J :
HEARD J.
SAMAHA R.
PILGRIM M.
                                                                  CREELMAN
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; 2000US-0197899.
; 2000US-0227439.
                                                                                                                                             2000WO-US31344.
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                                                                            BIOTECHNOLOGY
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/product=
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                                                                                                                                                                                                             "Transcription
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                                                                                                                                                                                                              factor,
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                                                                                                                                                                                                                                                                                                    element;
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                           Alignment Scores:
                                                                                                                                                               The present sequence is Arabidopsis thaliana transcription factor, CC G1324 cDNA. The transcription factor is used for altering a plant's CC biochemical characteristics. The transcription factor may be used to calter the structure and developmental characteristics of plants such as cybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, CC alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry, craspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, CC grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers, CC pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, CC pineapple, spinach, squash, sweet corn, transcription factors are CC key controlling elements of biological pathways and altering expression CC levels of 1 or more transcription factors can change entire biological pathways in an organism. Therefore manipulating transcription factor CC levels in plants offers great potential in agricultural biotechnology CC for modifying a plant's traits. Transcription factor CDNA is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn, potato and cotton plants -
                                                                                                                        Sequence 1137
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 87-88; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Creelman R,
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US-10-021-811-36 (1-206) x AAD05784 (1-1137)

Indels: Gaps:

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                                                                                       GlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGlnLysHisIleLys
                                                                                                                        IleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLysIleAlaLysHisLeuPro
                                                                                                                                                                                                                                                   AsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTrp
                                                                                                                                                                                                                                                                             ACTITIGAGGAGACACACTICTCACAAATTACATCCICCATAACGGTGAGGGTCGTTGG
                                                                                                                                                                                                                                                                                               ThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHisGlyGluGlyValTrp
                                                                                                                                                                                                                                                                                                                                  ATGAAGAAGAAGAAGACTTCAAAGAAAGTGAAGATGAAGAACTAAGAAGAGGGCCTTGG
SerThrSerHisValSerThrMetAlaGluProMetGluMetTyrSerProProCysTyr
                                             GlnAlaGluAsnPheGlnGlnGlnSerSerAsnAsnSerGluIleAsnAspHisGlnAla
                                                                        GGAAGAACGGATAACGAGATCAAGAACTATTGGAGAACAAGAGTTCAAAAAACAAGCTCGT
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                        TCTAACAGCGACAAGTTCTTTGAC--
                         -GCTGTT
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         The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2000;
16-NOV-2000;
16-APR-2001;
                                                                                                                                                                          Claim
                                                                                                                                                                                                                                   An isolated or recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                (RATC/)
(REUB/)
(RIEC/)
(YUGG/)
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(KEDD/)
(ADAM/)
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(PILG/)
(CREE/)
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JIANG C.
KEDDIE J.
ADAM L.
RATCLIFF O.
REUBER J L.
RIECHMANN J I
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Ratcliff O,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC exhibits ectopic expression or altered expression of one or more genes CC associated with a plant trait as compared to a wild plant. Also included CC are a transgenic plant comprising the polynucleotides, a computer CC readable medium having stored sequence information, and identifying a CC homologue sequence from a database comprising plurality of known plant sequences comprising inputting sequence information. The isolated or CC 464 fully defined sequences given in the specification. The isolated or CC recombinant polynucleotide is used for producing a plant having a CC modified trait, the method comprising selecting a polynucleotide that CC encodes a polypeptide or an antisense nucleic acid, inserting the CC polynucleotide or antisense nucleic acid into an expression vector, CC introducing the vector into a plant or a cell of a plant to overexpress CC plant, and selecting for a modified trait (e.g. increased CC production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial CC disease resistance, herbicide resistance, seed and fruit yield, growth cCC recoding an A. thaliana transcription factor.
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                             GluMetTyrSerProProCysTyrGlnGlyMetLeuGluProPheSerThrGlnPhePro
                                                              TTCGTGATCAACAACAAC
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RESULT 10
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       The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thallana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phantotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                                               Claim 4;
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(ADAM/)
(RATC/)
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JIANG C.
KEDDIE J.
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Ratcliff O, R
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YU G.
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DUBELL A J.
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Reuber JL, Riechmann
comprising the polynucleotides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          combined sequence from a database comprising a plurality of known plant compression inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or combinant polynucleotide is used for producing a plant having a commodified trait, the method comprising selecting a polynucleotide that commodes a polypeptide or an antisense nucleic acid, inserting the color polynucleotide into a plant or a cell of a plant to overexpress for vector, comprising the vector into a plant or a cell of a plant to overexpress components of the polypeptide or antisense nucleic acid, thereby producing a modified component of agriculturally useful proteins or metabolic chemicals, components to environmental stress response (e.g. drought), microbial contacts and flower sensescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides contacts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCys
     AspAsnAsnAsn---IleAsnTyr
                                                                   GluProPheSerThrGlnPheProThrIleAsnProAspGlnSerSerCysCysThrAsn
                                                                                                       GCAGCCACC-----
                                                                                                                                    ValSerThrMetAlaGluProMetGluMetTyrSerProProCysTyrGlnGlyMetLeu
                                                                                                                                                                    AAGCATGCGAAACAGTTGAAATGTGATGTGAATAGCCAACAATTCAAAGACACAATGAAG
                                                                                                                                                                                                                                                              LysHisIleLysGlnAlaGlu------
                                                                                                                                                                                                                                                                                                 CAATATTTACCGGGAAGAACGGACAACGAGATCAAGAACTACTGGAGGACGCGGGTGCAA
                                                                                                                                                                                                                                                                                                                      GAACAACTCTTGATCCTCGAACTTCATTCCCGTTGGGGAAATAGATGGTCAAAAATCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                  AGACTAAGGTGGTTAAACTATCTCCGCCCTGACGTCCGCCGTGGAAACATTACACTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGGTCGCTGGAACTCTCTTTCTCGTTGCGCCCGGCCTCCAACGCACCGGTAAAAAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAGGTCCGTGGACTGCTGAAGAATTTTAAGCTCATGAATTACATTGCTACTAATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGATGANAAGGGAAGAAGCTTGAAGAACAACATGGAAGACGAGATGGACCTNAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetAspLysLysGlnGlnCysLysThrSerGlnAspProGlu------ValArg
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                                       -- ACAACCACCACCACCAGGATCAGCCGGCACGTCATCTTGCATCACAACC 543
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544

TCTAACAATCAATTCATGAATTAC

567

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Alignment & Pred. No.: Score:
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Query
DB:
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AAH87724
ID AAH87
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                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                US-10-021-811-36 (1-206) x AAH87724
                                                                                                                                                                                                                                                                       The invention relates to nucleic acid molecules (AAH87645-AAH88116) the correspond to all or part of a mRNA molecule expressed in plant oil gland cells, especially peppermint and plant oil glands that produce terpenoid essential oils and resins. The nucleic acids are useful for genetically mapping a plant genome for genes expressed in plant oil gland cells and to suppress (for example by antisense suppression) or enhance their expression (for example by genetically transforming a plant cell with a replicable expression vector that expresses one or moroteins naturally expressed in plant oil gland cells). The nucleic acid are also useful for recombinant expression of plant oil gland proteins required for terpenoid essential oil and/or resin production in bacteri and/or yeast cells.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488706/53.
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                                                                                                                                                                                                                                                   Sequence 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                              peppermint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JAN-2000;
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                                  AnnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTrp
                                                                                                         GlnCysLysThrSerGlnAspPro-----
                                                 ThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHisGlyGluGlyValTrp
                                                                                   Scores:
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LANGE B M.
WILDUNG M R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              c acid molecules
oil glands for
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                                                                                                                                                                                                                                                  BP; 187 A; 158
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57.31%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              s corresponding to mRNA molecules expressed in enhancing expression of plant oil gland cell
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Matches:
Conservative:
Mismatches:
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Gaps:
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RESULT 1:
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The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant.
                                                                                                                                                                                                                                                                    New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant; transcription factor; gene expression; eucalyptus; pine; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAR-1999;
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-2000; 2000WO-US06112.
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                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eucalyptus grandis.
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type 2 Cys2His2; CCAAT box element; MYB; ss.
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99US-0149485.
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Match:

Percent Similarity:

Local

Similarity:

5.31e-43 475.00 66.48% 51.40% 41.74%

Conservative: Mismatches: Indels:

Length: Matches:

Score:

No.:

US-10-021-811-36 (1-206) x AAX25572

(1-837)

Gaps:

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CC This is the sequence of Arabidopsis thaliana ecotype C24 cDNA CC encoding the stress-related protein AtMYB2 (see AAY05831). The CC cDNA was obtained by RT-PCR of anaerobically induced root RNA CC derived from ecotype C24. The inventors have demonstrated that a CC capable of inducing the expression of stress-related genes in plant CC capable of inducing the expression of stress-related genes in plant CC cells in response to stress situations. The MYB2 protein encoded CC by the AtMYB2 gene is useful for the purposes of inducing or repressing the expression of plant-expressible genes that are CC involved in the plant's response to anaerobic stress, flooding CC stress, cold stress, dehydration stress, drought stress, flooding CC stress or salinity. The stress-related gene, such as the CC alcohol dehydrogenase Adhl gene, is transactivated by the MYB2 CC polypeptide by virtue of the presence of at least one copy of a CC cis-acting regulatory sequence, in particular a MBS-1 (Myb binding CC site) motif and/or a GC-motif and/or a GC-motif and/or a G-box-1 motif and/or a GC-motif and/or a G-box-1 motif and/or a GC-motif and/or a GP-box-1 motif and/or a GC-motif and/or a GP-box-1 motif and/or a GC-motif and/or a GP-motif and
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Alignment Sequence 837 BP; Scores: 246 A; 176 Ω; 212 ç. 203 T,

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맑 S 밁 Ś 뮹 Ś S 밁 Ś 밁 5 멍 S 밁 S 밁 115 235 175 91 71 51 31 55 11 GAAGATTCTGATGTACGGAAAGGTCCATGGACCGAGGAAGAAGATGCAATCCTAGTCAAC GlnAspProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsn TCATTACCCACCACGTGTGAACAAGTGGAGTCAATGATCACCGACCCAAGTCAACCAGTT GlnAlaSerThr----GlnGlnGlnSerSerAsnAsn-TrpArgThrArgIleGlnLysHisIleLysGlnAla------GluAsnPhe AGGTGGTCGAAGATTGCGCAATATCTACCGGGAAGAACAGATAATGAAATAAAGAATTAT ArgTrpSerLysIleAlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyr 110 GGCAACATCACTCTCGAAGAACAATTTATGATCCTCAAACTCCATTCTCTTTGGGGCAAT GlyAsnIleThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLySTrpGlyAsn CGAACTGGTAAGAGTTGTAGATTAAGATGGCTTAATTACCTTACGTCCAGATGTTAGAAGA ArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArg TICGICITATICATGGCGATGCTCGTTGGAACCACATCGCTCCTCTGGGCTAAAG TyrIleAlaAsnHisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLys TTCAAGGAGACTATGAGAAATGTTTGGATGCCGAGATTAGTGGAACGAATCAACGCCCAA TGGAGAACTCGAGTCCAAAAGCAAGCCAAACACCTAAGATGCGATGTTAACAGTAATCTT SerHisValSerThrMetAlaGluProMet 152 -SerGluIleAsnAspHis 90 114 534 474 414 125 354 294 234 70 174 50

	17-JUN-1999;	16-JUN-1999;	14-JUN-1999;	10-JUN-1999;	10-JUN-1999;	08-JUN-1999;	07-JUN-1999;	04-JUN-1999;	01-JUN-1999;	28-MAY-1999;	27-MAY-1999;	25-MAY-1999;	24-MAY-1999;	20-MAY-1999;	19-MAY-1999;	18-MAY-1999;	14-MAY-1999;	14-MAY-1999;	14-MAY-1999;	14-MAY-1999;	17-MAY-1999;	06-MAY-1999;	06-MAY-1999;	05-MAY-1999;	04-MAY-1999;	30-APR-1999;	28-APR-1999;	23-APR-1999;	23-APR-1999;	21-APF-1999;	19-APR-1999;	16-APE-1999;	06-APE-1999;	01-APF-1999;	29-MAF-1999;	25-MAE-1999;	73-MAE-1999;	05-MAF-199	25-FEE-1999;	XX XX		PD 06-SEP-2000.	PN EP1033405-A2.	•	Arabidonsis thaliana	metabolic pathway; promoter; termination se	identifica		DE Arabidopsis thaliana DNA fragment SEO ID NO: 44531.	DT 18-OC:-2000 (first entry)		AC AAC44894:	ID AAC44894 standard, DNA; 959 BP.	AAC44894		Db 535 AACGAACCGAGTCCGGTCGAGCCGGGTTTCGTTCAATTC 573			
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Alignment S
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                                                                                                                                                                                                                                                                                    TyrTrpSerMetGlu 195
                                                                                                                                                                                                                              standard; DNA;
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plant; transcription factor; gene expression; eucalyptus; plne; acacipoplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeodox; homeodomain; homeodox; MADS; homeodomain zipper; LIM domain; AP2; EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.
                                                                                                                                                                                                                                                                                                                          Eucalyptus grandis transcription factor DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSer
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and ERBES, zinc finger domains of type 2 Cys2His2, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 389 BP; 112 A; 102 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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 284
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                                                                                                               AGTTGGAACTCCCTÁGCCÁAÁGCTGCTGGTCTÁAÁAÁCGTACCGGGÁÁGAGTTGTCGGCTC
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CTCCTGATCATGGAACTGCATGCCAAGTGGGGAAACAGG
                                                                                                                                                                                        ProTrpThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHisGlyGluGly 38
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FLETCHER CHALLENGE FORESTS LTD.
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Search completed: February Job time : 226 secs

8, 2003, 11:12:19

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-Q-/cgn2 1/USPTO_spool/US10021811/runat_03022003_111222_25655/app_query.fasta_1.391
-DB=Issued_Patents NA -QFMT=fastap -SUFFIX=rni -MINMAYCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Ygapop 10.0
Fgapop 6.0
Delop 6.0
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Match
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1138
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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45 summaries
     US-08-997-251-1
US-08-997-251-3
US-08-927-2626B-1
PCT-US93-06251-90
US-08-306-691B-45
PCT-US93-06251-91
PCT-US93-06251-91
PCT-US93-06251-91
US-09-167-322-10
US-09-402-929-5
US-09-402-929-1
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Sequence 3, Appli
Sequence 1, Appli
Sequence 90, Appl
Sequence 45, Appl
Sequence 89, Appl
Sequence 89, Appli
Sequence 10, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
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13 248 21.8 4059 2 US-08-485-139-1 Sequence 1, Appli 14 248 21.8 4059 3 US-08-750-357-5 Sequence 5, Appli 16 248 21.8 4824 3 US-08-750-357-5 Sequence 5, Appli 17 185.5 16.3 469 3 US-09-400-618-2 Sequence 2, Appli 185.5 16.3 469 4 US-09-400-618-2 Sequence 2, Appli 185.5 16.3 469 4 US-09-400-618-2 Sequence 2, Appli 185.5 16.3 469 4 US-09-400-618-2 Sequence 2, Appli 195.5 11.0 785 3 US-09-008-979A-6 Sequence 2, Appli 20 165.5 11.0 785 3 US-09-008-979A-6 Sequence 6, Appli 21 11.0 785 3 US-09-008-979A-6 Sequence 6, Appli 22 11.0 785 4 US-09-460-618-6 Sequence 6, Appli 22 11.0 785 4 US-09-156-316-11 Sequence 11, Appli 22 11.0 5 2837 4 US-09-156-316-11 Sequence 11, Appli 23 11.6 4 US-09-156-316-11 Sequence 11, Appli 25 105.5 9.3 1116 4 US-09-280-590A-17 Sequence 11, Appli 25 105.5 9.3 2903 4 US-08-928-941D-17 Sequence 2, Appli 26 105.5 9.3 2903 4 US-08-928-941D-2 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 2, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 105, Appli 30 105.5 9.3 3767 4 US-09-280-590A-3 Sequence 105, Appli 30 105.5 9.3 3627 1 US-08-454-0056-13 Sequence 23, Appli 30 105.5 9.3 3627 1 US-08-454-0056-23 Sequence 23, Ap
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## ALIGNMENTS

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WESULT 1

US-08-997-251-1

Sequence 1, Application US/08997251

Sequence 1, Application US/08997251

Patent No. 6271440

GENERAL INFORMATION:

APPLICANT: JACOBSEN, JOHN V.

APPLICANT: JACOBSEN, JOHN V.

APPLICANT: JACOBSEN, JOHN V.

TITLE OF INVENTION: PLANT REGULATORY PROTEINS III

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS: 17

CORRESPONDENCE ADDRESS: 17

CORRESPONDENCE ADDRESS: 17

CORPESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Boulevard

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/997,251

FILING DATE: 23-DEC-1997

CLASSIFICATION NUMBER: WO AU96/00383

FILING DATE: 21-DUN-1996

PRIOR APPLICATION NUMBER: AU PN6470/95

FILING DATE: 09-NOV-1995

PRIOR APPLICATION NUMBER: AU PN6470/95

FILING DATE: 23-JUN-1996

PRIOR APPLICATION NUMBER: AU PN6470/95

FILING DATE: 23-JUN-1995

PRIOR APPLICATION NUMBER: AU PN6470/95

PRIOR APPLICATION NUMBER: AU PN64
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Best Local Similarity:
Query Match:
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; LOCATION:
US-08-997-251-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Sequence 3, Application US/08997251
Patent No. 6271440
GENERAL INFORMATION:
APPLICANT: GUBLER, FRANZ J.
APPLICANT: JACOBSEN, JOHN V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 28,547
REFIRENCE/DOCKET NUMBER: 110-
TELECOMMUNICATION INFORMATION:
TELIFPHONE: (303) 499-8080
TELIFPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPCLOGY: line MOLECULE TYPE: CORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 FroGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyrIle
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DEVELOPMENTAL STAGE: Seed
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TYPE: nucleic acid
STRINDEDNESS: single
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                                                                                                                                                                                                                                                                                                 GCTCGGATGGCCGCTCATTTGCCAGGGCGTACTGATAATGAAATAAAGAATTACTGGAAC 691
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Indels:
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Best Local Similarity:
Query Match:
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APPLICATION UNMBER: US/08/997,251
FILING DATE: 23-DEC-1997
CLASSIFICATION UNMBER: US/08/997,251
FILING DATE: 23-DEC-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: WO AU96/00383
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN6470/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN6470/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN3779/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN3779/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10-97
TELECOMMUNICATION NUMBER: 110-97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (303) 499-80
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PLANT REGULATORY PROTEIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Greenlee, Winner and Sullivan,
STREET: 5370 Manhattan Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2352 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
687 TTCACCGCCGAGGAGGAGAGGCTCATCATCCAGCTCCACCTCCAAGATGGGGAACAAGTGG
                                                                                                                                                     567 AAGAAGCACGGCGAGGGGAACTGGAACGCGGTGCAGAAGAACACCGGGGCTGTTCCGGTGC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                 GlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArgGlyAsn
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                                                                                                                                                                                                                                CCCCCGCTGAAGAAGGGGCCATGGACGTCGGCGAGGACGACCCATCCTGGTGGACTACGTG
                                                                                                                                                                                                                                                         ProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyrIle
                                 IleThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTrpGlyAsnArgTrp
                                                                          GGCAAGAGCTGCCGCCTCCGGTGGGCGAACCACCTGAGGCCCCAACCTCAAGAAGGGGGCCC
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33.92%
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Matches:
Conservative:
Mismatches:
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Gaps:
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68
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746
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US-08-722-626B-1
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   Query Match:
              Percent Similarity:
Best Local Similarity:
                                                                             Alignment Scores:
                                                                                                           US-08-722-626B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Yang, Yinong
APPLICANT: Klessig, Dav
                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                        FEATURE:
NAME/KEY: Coding S
LOCATION: 148...98
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/722,626B
FILING DATE: 27-SEP-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Klessig, Daniel, F.
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
                                                           . No.:
                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 215 563-4100
TELEFAX: 215 563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                          ENGTH:
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1601 Market Street Suite 720
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PCT-US93-06251-90
                                                                                                                                                                                                                                                                                                                                                                             Sequence 90, Application PC/TUS9306251 GENERAL INFORMATION:
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
                                                                                                                                                                                                                                                                                                                       APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION
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               FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                              COUNTRY: US
ZIP: 11530
                                                                                                                                                                                                                STATE:
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                                                   PCT/US93/06251
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NAM3: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 85

8586

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; Sequence 45, Application U;
PATENT NO. 5734039
; GENERAL INFORMATION:
APPLICANT: Calabretta,
APPLICANT: Skorski, To
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US-08-306-691B-45
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Best Local Similarity:
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PCT-US93-06251-90
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TELESPHONE: 516-742-4343
TELESTAX: 516-742-4366
TELESX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 1035 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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    Calabretta, Bruno
Skorski, Tomasz
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Pred. No.:
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LENGTH: 3225 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/306,6:
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
7TD. 10102
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                       AGATGGGCAGAAATCGCAAAGCTACTGCCTGGACGAACTGATAATGCTATCAAGAACCAC
                                                                                                                                                    actictigacagaagagaagacagaattatttaccaggcacacaagagactiggggaac
                                                                                                                                                                            GlyAsnIleThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTrpGlyAsn
                                                                                                                                                                                                                ArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArg
                                                                                                                                                                                                                                                                                                         IleAlaAsnHisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLys---
AsnAsnSerGlu-----IleAsnAspHisGlnAlaSerThrSerHisValSerThrMet 148
                                                TrpArgThrArgIleGlnLysHisIleLysGlnAlaGluAsnPheGlnGlnGlnSerSer
                                                                                                            ArgTrpSerLysIleAlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyr
                                                                                                                                                                                                                                                                              GTACAGAAATACGGTCCGAAACGTTGGTCTGTTATTGCCAAG-----CACTTAAAGGGG 485
                             TGGAATTCTACAATGCGTCGGAAGGTCGAACAG---GAAGGTTATCTGCAGGAGTCTTCA
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IBM PS/2
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Matches:
Conservative:
Mismatches:
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RESULT 6
PCT-US93-06251-91
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                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                              score:
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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723 AAAGCCAGCCAGCAGTGGCCACAAGCTTCCAGAAGAACAGTCATTTGATGGGTTTT
   432
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NAME: DiGiglio, Frank S.
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                   32
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                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3225 LENGTH: 3225 Cold
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TELEFAX: 516-742-4366
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                                  IleAlaAsnHisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLys---
                                                                     AACCCTGAGCTCATCAAGGGTCCTTGGACCAAAGAAGAAGATCAGAGAGTGATAGAGCTT 431
                                                                                                  AspProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyr
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Matches:
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PCT-US93-06251-89
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                                                                                        TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930627
CLASSIFTT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
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                                    STRANDEDNESS:
                                                   TYPE: nucleic acid
                                                                                                                                             TELEPHONE: 516-742-43
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAATTGGAAAACAATGTAGGGAGAGGTGGCATAACCACTTGAATCCAGAAGTTAAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATGGGCAGAAATCGCAAAGCTACTGCCTGGACGAACTGATAATGCTATCAAGAACCAC
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   DNA (genomic)
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RESULT 8
US-09-167-322-10
; Sequence 10, Application
; Patent Nc. 6365151
; PATENT NC. 1NFORMATION:
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Pred. No.:
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COMPUTER READABLE FORM:
MEDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                        NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  AFPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S. England, James M. TITLE OF INVENTION: CANCER VACCINE
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                                                                                  STATE: PA
COUNTRY: USA
ZIP: 19102
                                                                                                                          ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, STREET: Suite 1800, Two Penn Center Plaza CITY: Philadelphia
                                                                                                                                                                                                                                                                                                 Application US/09167322
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Best Local Similarity:
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LENGTH: 1897 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 79:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US97/00582 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/167,322
APPLICATION OFF-1998
FILING DATE: 07-Oct-1998
CLASSIFICATION: «Unknown»
                              GlnPhePro----
                                                                                                                                                      MetAlaGluProMetGluMetTyrSerProProCys-----------
                                                                                                                                                                                      AAAGCCGGCCCGCCCTCGGCAACCACCGGCTTCCAGAAGAGC---AGCCATCTGATGGCC
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CAGATCCCATATCCAGTAGCACTGCATATAAATATTÄTCÄÄTGTTCCTCAGCC-AGCTGC
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                                                             GCCCCTCTGGGCAGTGACTACCCCTACTACCACATTGCTGAGCCACAAAATGTCCCTGGT
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TELEFAX: (215) 568-5549
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Temple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4880 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
71 GlyAsnIleThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTrpGlyAsn 90
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                                                                                                                                                                                                           12 AspProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyr 31
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                                                                                                       GTTCAGAAATATGGGCCAAAAAGATGGTCTTTAATTGCAAAA-----CATTTAAAAGGA 461
                                      AGAATAGGCAAGCAGTGTAGAGAAAGATGGCATAATCATCTGAATCCTGAGGTAAAGAAA
                                                                 ArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArg 70
                                                                                                                                                                           AATCCTGAATTGATAÁAGGGTCCTTGGACTAAAGÁAGAAGATCAGAGGGTTATTGAATTA 407
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Hatton, Kimi
Reddy, E. P.
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US-09-402-929-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6410825
GENERAL INFORMATION:
                                                                                    TELEFAX: (215) 568-5549 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-8383
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                            LENGTH: 3602 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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               STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                              NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEIDEL,
STREET: Suite 1800
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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Hatton, Kimi
Reddy, E. P.
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Two Penn Center Plaza
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Temple University - Of The Commonwealt:
APPLICANT: Toscani, Anconio
APPLICANT: Hatton, Kimi
APPLICANT: Reddy, E. P.
TITLE OF INVENTION: B. P.
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                       patent No. 6410825
                                                                        COMPUTER READABLE FORM:
MEDIDIM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,929
             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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FILING
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REGISTRATION NUMBER: 30,480
REFERENCE, DOCKET NUMBER: 6056
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEPAX: (215) 568-8383
TELEPAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                     Sequence 46, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING
NUMBER OF SEQUENCES: 55
                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna
STREET: Two Penn Center, Suite 1800
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                                                                                                                                                                                                                                                                                                                                                   147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 AspProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyr 31
CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTCCTGGACAGAAGAAGACAGGATCATATATGAAGCACACAAGCGCCTGGGAAAAC 3982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyAsnIleThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTrpGlyAsn 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCAGAAATATGGGCCAAAAAGGTGGTCTTTAATTGCAAAA-----CATTTAAAAGGA 3862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleAlaAsnHisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLys--- 50
                                                                                                                                                                                                                                                                                                                                                                                 TCAGAGCGGTCTTCATCAAAACTTCAACACAAACCTTGTGCGACTATGGACCATTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATCCAGAATTGATAAAGGGTCCTTGGACTAAGGAAGAAGATCAGAGGGTTATTGAATTA 3808
                                                                                                                                                                                                                                                                                                               ACCCAG-----AATCAGTTTTACATTCCTGTTCAGATCCCTGGGTATCAG 4207
                                                                                                                                                                                                                                                                                                                                                                                                                         SerSerAsnAsnSerGluIleAsnAspHisGln-----AlaSerThrSerHisValSer 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrpArgThrArgIleGlnLysHisIleLysGlnAlaGluAsnPheGlnGln-----Gln 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTTGGGCCGAGATTGCTAAGTTACTTCCTGGAAAGGACTGATAATTCTATCAAAAATCAT 4042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgTrpSerLysIleAlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyr 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAATAGGCAAGCAGTGCAGAGAAAGATGGCACAATCACCTGAACCCTGAAGTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArg 70
                                                                                                                                                                                                                                                                                                                                                 ThrMetAlaGluProMetGluMetTyrSerPro-----ProCysTyrGln 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAATTCTACCATGCGAAGAAAAGTGGAACAGGAGGGCTATTTACAAGATGGAATAAAA 4102
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Matches:
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DB:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/306,69
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                                                                                                                                                                                                                                                                                                                                                                                                                                              41 AsnSerLeuAlaLysAlaAlaGlyLeuLys---ArgAsnGlyLysSerCysArgLeuArg 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GlnGlnCysLys-----ThrSerGlnAspProGluValArgLysGlyProTrp
                                                                                                                                                                                                                    ProGlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGlnLysHisIle 119
GluMetTyrSerProProCysTyrGlnGlyMetLeuGluProPheSerThrGlnPhePro
                                                       ---GlulleAsnAspHisGlnAlaSerThrSerHisValSerThrMetAlaGluProMet 152
                                                                                                                           ---GACACAGGAGGCTTCTTGAGCGAGTCCAAAGACTGCAAGCCCCCAGTGTACTTGCTG
                                                                                                                                                            LysGlnAlaGluAsnPheGlnGlnGlnSerSerAsnAsnSer------- 133
                                                                                                                                                                                              ATCATCTGCGAGGCCCACAAGGTGCTGGGCAACCGCTGGGCCGAGATCGCCAAGATGTTG
                                                                                                                                                                                                                                                                                          LeuIleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLysIleAlaLysHisLeu
                                                                                                                                                                                                                                                                                                                                     TGGCACAACCACCTCAACCCTGAGGTGAAGAAGTCTTGCTGGACCGAGGAGGAGGACCGC 559
                                                                                                                                                                                                                                                                                                                                                                        TrpLeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeu 79
                                                                                                                                                                                                                                                                                                                                                                                                             ACACTGATTGCCAAG-----CACCTGAAGGGCCGGCTGGGGAAGCAGTGCCGTGAACGC 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCAAAGAGGAAGACCAAAAAGTCATCGAGCTGGTTAAGAAGTATGGCACAAAGCAGTGG
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271.50
52.17%
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23.86%
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4059 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KREBBERS, Enno
APPLICANT: WILLIAMS, Mark
APPLICANT: LEEMANS, Jan
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: MALE STERILE PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: I ORIGINAL SOURCE:
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 279..284
OTHER INFORMATION:
FEATURE:
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NAME/KEY:
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                                                                                                          FEATURE:
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LOCATION: 1505..1510
OTHER INFORMATION: /label=
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LOCATION:
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                                                                                                                                    LOCATION: 2081..2086
OTHER INFORMATION: /label=
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OTHER INFORMATION: /label= EcoRI
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LOCATION: 2418..2430
OTHER INFORMATION: /
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                                                                     NAME/KEY:
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P.O. Box 1404
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1230 TIATTTCATTTTGGGATCATATATATACCCCCGAGGCAAGACCGGAGGACGATCACGTGT 1289
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LOCATION: 1062
COTHER INFORMATION: /label= transcript-init
OTHER INFORMATION: /note= "transcription initiation site"
FEATURE:
NAME/KEY: intron
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NAME/KEY:
LOCATION: 2669..2674

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OTHER INFORMATION: /label= C1
OTHER INFORMATION: /note= "coding region of C1
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LOCATION: 3008..3013
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LOCATION: 2135..2430

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/note= "region containing polyadenylation signal
of C1 gene"
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/note= "TGCAG sequence (in C1 gene) which in
C1-S sequence is changed to TTAGG"
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/note= "region containing promoter of C1
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                                                                                                                                                                            TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4059 base pairs
                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: US/08/750,357 FILING DATE: 21-MAR-1997 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
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FEATURE:
NAME/KEY:
                                                                          FEATURE:
                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                   NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: USE OF
TITLE OF INVENTION: MALE ST
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APPLICANT: WILLIAMS, Mark
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                           LOCATION: 279..284
OTHER INFORMATION:
                                                           NAME/KEY:
                                                                                       ORGANISM:
                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia COUNTRY: United States ZIP: 22313-1404
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; LOCATION: 935..939
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NAME/KEY:
LOCATION: 2135..2430
OTHER INFORMATION: /la
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5880331
GENERAL INFORMATION:
                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LEEMANS, Jan
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: MALE STERILE PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1589 GCAGGCAGGCTGCCTGGCCGAACAACAATGAAATCAAGAACTACTGGAACAGCACGCTG 1648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1290 GTGGGTGCAGGTTTGCGTCGGTGCGGCAAGAGCTGCCGGCTGCGGTGGCTGAACTACCTC
TELECOMMUNICATION INFORMATION:
                  NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                               CITY: Alexandria
STATE: Virginia
COUNTRY: United States
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                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 ---AlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrLeu
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Gaps:
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COCATION: 2367..2379
COCATION: 2367..2379
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FEATURE:
NAME/KEY:
LOCATION: 884..888
COTHER INFORMATION: /label= C1-S
OTHER INFORMATION: /note= "TGCAG
OTHER INFORMATION: replaced with 'US-08-485-139-5
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4824 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 396..401
OTHER INFORMATION: ,
FEATURE:
NAME/KEY: -
LOCATION: 2367 2379
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     1538
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                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: cir
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                              1299
                                                                                                                                                                                                                                          ORGANISM: plasmid pCOL9 FEATURE:
                           96
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AlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIle 115
                                                                                                                                                                                                                                                                                                                                                           GCTGACGACGAGCGATCGATCGAGCGTCTGCTGCGAATTCATCTGTTCCGGTGTCGGCC 1478
                                                                                                                                                                                                             ArgProAspValArgArgGlyAsnIleThrProGluGlnLeuLeuIleMetGluLeu
                                               GIGTGAGAGTGAGCTCATTCATATGTACATGCGTGTTGGCG-CGCAGGTGGTCGCTGATT 1537
                                                                                                                                                                                          GGCCCAACATCAGGCGCGCAACATCTCCTACGACGAGGAGGATCTCATCATCCGCCTC 1358
                                                                                                                                                                                                                                                                                          TTATTTCATTTTGGGATCATATATATACCCCCGGAGGCAAGACCGGAGGACGATCACGTGT 1238
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248.00
41.67%
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21.79%
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/note= "TGCAG (in C1) which in C1-S
replaced with TTAGG"
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                                                                  HisAlaLysTrpGlyAsnArgTrpSerLysIle 95
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Search completed: February 8, 2003, 12:30:35 Job time : 55 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USTTO spool/US10021811/runat 03022003 111222 25671/app query.fasta_1.391
-DB=published Applications NA -QFMT=fastap -SUFFTX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10021811 @GCN 1 1 33 @Frunat 03022003 111222 25671
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WĀLT -LONGLOG
-DEV TIMEOUT=120 -WĀRN TIMEOUT=30 -THREADS=1 -XGAPOF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                            Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     1138
1062
874.5
829.5
                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq
                                                                                                                                                                                                                                          Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
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| length:
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Match
     100.0
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76.8
72.9
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1138
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   US-10-021-811-35
US-10-021-811-29
US-10-021-811-37
US-10-021-811-33
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1627.410 Million cell updates/sec
 Sequence 35,
Sequence 29,
Sequence 37,
Sequence 33,
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Pred. No.:
                                 Score:
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509 53.5 382 10 US-09-878-574-1305 Sequence 1305, Appli 55.9 55.6 392 10 US-09-878-574-33 Sequence 33, Appli 56.5 49.4 375 10 US-09-878-574-5021 Sequence 33, Appli 56.5 49.3 379 10 US-09-878-574-5021 Sequence 327, Appli 56.5 49.3 379 10 US-09-878-574-5025 Sequence 327, Appli 56.5 49.3 379 10 US-09-878-574-502 Sequence 194, Appli 56.5 49.4 36.5 10 US-09-878-574-505 Sequence 194, Appli 56.5 49.4 36.5 10 US-09-878-574-505 Sequence 194, Appli 56.5 49.7 36.5 10 US-09-878-574-505 Sequence 194, Appli 56.5 49.7 36.5 10 US-09-878-574-50 Sequence 194, Appli 56.5 49.7 36.5 10 US-10-021-811-9 Sequence 24, Appli 56.5 49.7 36.5 10 US-10-021-811-9 Sequence 24, Appli 56.5 49.7 36.5 10 US-10-021-811-9 Sequence 2390, Appli 56.5 44.2 34.8 9 US-10-021-811-19 Sequence 2390, Appli 49.4 34 10.1 186 9 US-10-021-811-9 Sequence 2390, Appli 49.4 34 10.1 186 9 US-10-021-811-9 Sequence 2390, Appli 49.5 40.3 81.0 9 US-10-021-811-9 Sequence 2390, Appli 49.5 40.5 86.7 10 US-09-938-842A-2390 Sequence 2390, Appli 49.5 40.5 86.6 10 US-09-938-842A-2393 Sequence 2390, Appli 49.5 40.5 86.6 10 US-09-938-842A-2393 Sequence 2294, Appli 49.5 40.5 86.6 10 US-09-938-842A-2393 Sequence 2294, Appli 49.5 86.5 77.9 9US-09-938-842A-2393 Sequence 2292, Appli 49.5 86.5 77.9 9US-09-938-842A-2393 Sequence 2390, Appli 39.4 51.4 10 US-09-938-842A-2393 Sequence 2390, Appli 39.4 51.4 10 US-09-938-842A-2393 Sequence 2390, Appli 39.7 16.6 9US-09-938-842A-2393 Sequence 2390, Appli 3
```

## ALIGNMENTS

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US-10-021-811-35

Sequence 35, Application US/10021811

Publication No. US20030024007A1

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Weng, Yiwen

APPLICANT: Weng, Zude

FILE REFERENCE: BB1294 US NA

CURRENT APPLICATION NUMBER: US/10/021,811

CURRENT APPLICATION NUMBER: US/10/021,811

CURRENT APPLICATION NUMBER: 60/110,609

PRIOR FILING DATE: 1998-December-02

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Microsoft Office 97

SEQ ID NO 35

LENGTH: B63

TYPE: DNA

ORGANISM: Glycine max

US-10-021-811-35

Alignment Scores:

Pred. No.:

Pred. No.:

Pred. No.:

1138.00

Best Local Similarity: 100.00%

Mismatches: 0
```

```
Sequence 29, Application US/10021811
Publication No. US20030024007A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Godell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Fargific Reference:
B11924 US NA
CURRENT FALLING DATE: 2001-12-14
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 1998-December-02
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOPTWARE: Microsoft Office 97
SEQ ID NO 29
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DB:
Alignment Scores
                              ; LENGTH: 988
; TYPE: DNA
; ORGANISM: Glycine max
US-10-021-811-29
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US-10-021-811-29
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Godell, Joan
APPLICANT: Fang, Yiwen
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Fac
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOPTWARE: Microsoft Office 97
SEQ ID NO 37
LENGTH: 805
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Publication No. US20030024007A1
GENERAL INFORMATION:
TYPE: DNA
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RESULT 4

US-10-021-811-33

i Sequence 33, Application US/10021811

publication No. US20030024007A1

i GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Odell, Joan

APPLICANT: Weng, Zude

ITILE OF INVENTION: Plant Myb Transcription Fac

FILE REFERENCE: BB1294 US NA

CURRENT APPLICATION NUMBER: US/10/021,811

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 60/110,609

PRIOR FILING DATE: 1998-December-02

"TMMHER OF SEQ ID NOS: 63
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Best Local Similarity:
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FEATURE:

NAME/KEY: unsure

LOCATION: (798)

NAME/KEY: unsure

LOCATION: (807)

NAME/KEY: unsure

LOCATION: (814)

US-10-021-811-33
US-09-878-574-1305

US-09-878-574-1305

; Sequence 1305, Application

; Patent No. US20020110548A1

; GENERAL INFORMATION:
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Best Local Similarity:
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SEQ ID NO 33
LENGTH: 910
TYPE: DNA
ORGANISM: Glycine max
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                                                            ATCTGGTCGTCTATGCAATTACTCAATGGAGAT
                                                                          SerTrp---SerMetGlnLeuLeuAsnGlyAsp
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829.50
83.89%
79.62%
72.89%
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Matches:
Conservative:
Mismatches:
Indels:
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US/09878574

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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Meng, Yiwen
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Hon
FILE REFIRENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILLING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER ON SEQ ID NOS: 63
SOFTMARE: Microsoft Office 97
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US-10-021-811-31
J Sequence 31, Application US/10021811
J Publication No. US20030024007A1
J GENERAL INFORMATION:
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DB:
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LENGTH: 382
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR PILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-039-Q1-B1-G9
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US-09-878-574-33; Sequence 33, Application US/09878574; Patent No. US20020110548A1
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NAME/KEY: ungure
LOCATION: (301)
NAME/KEY: ungure
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LENGTH: 530
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NAME/KEY:
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ORGANISM: Glycine
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arggaCAAGAAGCTTGGC---AACACGTCTCATGATCCTGAAGTGAGAAAGGGGCCATGG
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                                                             TTGCACAACCAATTGTCAACAATGGGCAACCCAAAAAAACTAATCTCA
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Matches:
Conservative:
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GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and FILE REFERNCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT APPLICATION NUMBER: 09/33,535
PRIOR APPLICATION NUMBER: 09/33,535
PRIOR FILING DATE: 199-06-14
PRIOR FILING DATE: 199-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Glycine n
; OTHER INFORMATION:
US-09-878-574-33
                                                                                                                                                                                                                                          RESULT 8
US-09-878-574-5021
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       Sequence 5021, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NIMBER OF CECT TO NOC. 15775
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SEQ ID NO 33
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Matches:
Conservative:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
FITTLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 327
LENGTH: 375
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Best Local Similarity:
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                                                                             ; TYPE: DNA; ORGANISM: Glycine m; OTHER INFORMATION: US-09-878-574-327
Percent Similarity:
Best Local Similarity:
                           Score:
                                        Pred.
                                                   Alignment Scores:
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APPLICANT: Byrum, Joseph R.
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ORGANISM: Glycine n
OTHER INFORMATION:
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: Clone ID: LIB3028-010-Q1-B1-B1
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80.58%
51.49%
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Matches:
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Sequence 3147, Application US/09878574
Patent Nc. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nuclèic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3147
LENGTH: 379
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Glycine max
THER INFORMATION: Clone ID: LIB3028-015-Q1-B1-E7
US-09-878-574-3147
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US-09-878-574-3147
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                            A:snSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTrp
          ANCTOTTTGGCCAACGCTGGTGGACTTAAACGTACCGGAAAGAGTTGCCGGCTCCGGTGG
                                                                         ACAATGGAAGATGACTTAATCTTGATCACCTATATTGCCAATCACGGGGAAGGGGTTTGG
                                                                                           ThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHisGlyGluGlyValTrp 40
                                                                                                                                      A regachagaagettege---aacaceteteateatecteaagteagaaagegeceateg
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560.50
89.17%
86.67%
49.25%
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Sequence 50, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Ha Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401) B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT PRICING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US/09/878,574
FILING DATE: 199-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 50
LENGTH: 350
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Best Local Similarity:
Query Match:
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; ORAULIM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(350)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-G4
US-09-878-574-50
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US-09-878-574-50
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             GlyArgThrAspAsnGluIleLysAsnTyrTrp 111
                                                                          IleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLysIleAlaLysHisLeuPro
                                                                                                                                       LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeuLeu
                                                                                                                                                                                                      AsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTrp
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                                                                                                                                                                                                                                                                                                                           MetAspLysLysGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTrp
                                                                                                                      CTAAACTACCTCCGTCCTGATGTTAGAAGAGGGAATATTACACCCGAGGAACAGCTTTTG
                                                                                                                                                                                   AACTCTTTGGCCAAGGCTGCTGGACTTAAACGTACCGGAAAGAGTTGCCGGCTCCGGTGG
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556.50
93.69%
92.79%
48.90%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-021-811-45

; Sequence 45, Application US/10021811

; Publication No. US20030024007A1

; GENERAL INFORMATION:
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; ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-054-Q1-B1-B1
US-09-878-574-194
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US-09-878-574-194
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SEQ ID NO 194
LENGTH: 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated 'TITLE OF INVENTION: Plants
FILE REFERENCE: 38-23(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION MUMBER: 09/333,535
PRIOR EPLING DATE: 1999-06-14
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: odel1, Joan
APPLICANT: odel1, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeuLeu
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545.50
93.64%
92.73%
47.93%
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Matches:
Conservative:
Mismatches:
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SOFTWARE: Microsoft Office
SEQ ID NO 45
LENGTH: 1236
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine r
FEATURE:
NAME/KEY: unsure
LOCATION: (519)
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LOCATION:
NAME/KEY:
LOCATION:
NAME/KEY:
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NAME/KEY:
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630 CAACCTTATACCACCAAATTCGAGGTTCTGAAT
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                      165 GlupropheSerThrGlnPheProThrIleAsn 175
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                                                                                                                                                                                                                              SerLysIleAlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyrTrpArg 112
                                                                                                                                                                                                                                                                                       GlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArgGlyAsn 72
                                                                                                                                                                                                                                                                                                                       -----CTTCGAAGAGGCCCTTGGACCGTCGATGAAGACCTCACTCTTATCAATTACATT
                                                                                                                                                                                                                                                                                                                                                                                  ProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyrIle 32
                                              GGCCCCCGTAACCACCACCGTAACTGCGGCCGCCACCAACAATGCATTCACCTACGGRAA
                                                                    GluProMetGluMetTyr---
                                                                                          GACACCATGNGNTACCTTTGNNATNCCAAGGCTCGTGGAACGCATTCAAGCAGCGGCGAC
                                                                                                                SerAsnAsnSerGluIleAsnAspHisGlnAlaSerThrSerHisValSerThrMetAla 149
                                                                                                                                     ThrArgIleGlnLysHisIleLysGlnAlaGlu-----AsnPheGlnGlnGlnSer
                                                                                                                                                                                                                                                                           GGGAAGAGTTGCAGATTGAGGTGGCTGAATTATCTGCGTCCTGATGTTCGACGTGGAAAC
                                                                                                                                                                                                                                                                                                                                  AlaAsnHisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsn 52
                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGATGAAAAAGGAGCAAGAAGTAGCAACACCCTTTTAAGTTGTGAGGACGAGATGGAC 155
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(534)
unsure
(800)
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(1151)
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(530)..
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528.00
68.06%
53.93%
46.40%
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Matches:
Conservative:
Mismatches:
Indels:
                                                                     -SerProProCysTyrGlnGlyMetLeu 164
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103
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US-10-021-811-17

Sequence 17, Application US/10021811

Publication No. US20030024007A1

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Fang, Yiwen

APPLICANT: Woell, Joan

APPLICANT: Odell, Joan

APPLICANT: Odell, Joan

APPLICANT: BAIST SUBJECT ON BEILD REFERENCE: BB1294 US NA

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: US/10/021,811

CURRENT FILING DATE: 1998-December-02

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Microsoft Office 97

SEQ ID NO: 17

TEMPORTY. EGS | 1998-December-02

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Microsoft Office 97
RESULT 15
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Best Local Similarity:
Query Match:
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LOCATION: (577)
NAME/KEY: unsure
LOCATION: (582)...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Oryza sativa 
FEATURE:
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                                                                                       GACGTCAACTCCCAGCAGTTCAAGGACCTCATGCGCTACCTCTGGATGCCCGCCTCCTCG
                                                                                                                       GluIleAsnAspHisGln-----
                             AACGCATCAACGCTC 484
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                                                                                                                                                                                     ArgIleGlnLysHisIleLysGlnAlaGluAsnPheGlnGlnGlnSerSerAsnAsnSer 133
                                                                                                                                                                                                                                       LysIleAlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyrTrpArgThr 113
                                                                                                                                                                                                                                                                                 ACGGCGAGGAGCAGCTGCTGATACTGGAGCTCCATGGGCGGTGGGGGAATCGGTGGAGC
                                                                                                                                                                                                                                                                                                      ThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCTCCGGCGAGGGCCGTGGACGGTGGAGGAGGAGGACCTGCTCCTCGTCAACTACATCGCC
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519.50
77.24%
64.83%
45.65%
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Matches:
Conservative:
Mismatches:
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Query Match:
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; ORGANISM: Glycine
US-10-021-811-47
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Pred. No.:
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Odell Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
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Sequence 47, Application US/10021811
Publication No. US20030024007A1
GENERAL INFORMATION:
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SEQ ID NO 47
LENGTH: 1181
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                                                                                                                                                                                                                                                                                                                       ThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGlnLys------HisIle 119
ThrIleAsnProAspGlnSerSerCysCys--
                                 CAGGGACCTTGTATGAATGAAGCTGGTCCCACTTACATGGACCAACATGAGCAGACTCAG
                                                                 GlnGly-----MetLeuGluProPheSerThr------
                                                                                                                              SerThrSerHisValSerThrMetAlaGluProMetGluMetTyrSerProProCysTyr 160
                                                                                                                                                                                                                                 AAAATTTACACTGACAGCAGAGAGTTTCAAGAACTTGTTAGGCGTTTCTGGATGCCTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                               TATCTAAAGCCAGATGTAAAACGGGGAAATTTAACCCCACAAGAGCAACTTATAATTCTT
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Search completed: Job time : 62 secs	B	8	뫄	Ś	р	გ	D	Ś	皮	ફ	망
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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10021811/runat_03022003_111222_25647/app_query.fasta_1.391
-Q=/cgn2_1/USPTO_spool/US10021811/runat_03022003_111222_25647/app_query.fasta_1.391
-DB=EST_QEMT=fastap_SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blts_START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=blts_START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10021811_GCGN 1 1349_grunat_03022003_111222_2567 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOPE10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

ACCESSION VERSION KEYWORDS LOCUS DEFINITION RESULT 1 BM732121 SOURCE ORGANISM sequence. BM732121 BM732121.1 EST. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; BM732121 562 bp mRNA linear EST 01-MAR-2002 sal73b11.y1 Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1061-4678 5' similar to TR:Q39028 Q39028 ATMYB2. ;, mRNA soybean. Glycine max Glycine. GI:19053454

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81 I..eMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLysIleAlaLysHisLeuPro
                                                                                                   61 LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeuLeu
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                                                                      C"AAATTACCTCCGTCCTGATGTTAGAAGAGGGAATATTACACCCGAGGAACAACTTTTG
                                                                                                                                                                                                                                                                      ACAATGGAAGAAGACTTGATCTTGATGAAACTATATTGCAAATCATGGGGAAGGTGTTTGG 139
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
7el: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This Clone 18 available through: ResGen, Invitrogen Corp. 2130
South Memorrial Parkway Huntsville, AL 35801 For further information
call: (800) 533-4363 or contact: ccu@resgen.com web site:
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="vector: pBluescript II SK+; Site_1: EcoRI; Site_2: xhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a xhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI. XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3847"
/clome="50YBEAN CLONE ID: Gm-c1061-4678"
/clone_lib="Gm-c1061"
/clone_type="mature flowers of field grown plants"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Glycine max"
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Boll46360.1 GI:20283419
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barrel medic.

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Trifolieae
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: gdmay@noble.org
Insert Length: 635 Std Error: 0.0
Plate: 047 row: E column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
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/note="Vector: Lambda Zap; cDNA was prepared from polyA+enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XII-Blue MRF' (Stratagene). Excised plasmids were plated
                                                                                                                                                                                                                          /clone="NF047E06FL"
/clone lib="Developing flower"
/tissue_type="Developing flowers"
/dev stage="Developmentally pooled. Contains
very young, developing, fully-opened flowers
in early transition into pods."
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|db_xref="taxon:3880"
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                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
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US-10-021-811-36 (1-206) x
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                                                                                                                                     LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeuLeu
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                         IleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLysIleAlaLysHisLeuPro
                                                                                                                                                                                                                 AATTCTTTGGCCAAAGCTGCTGGTCTCAAACGTACCGGAAAGAGTTGCCGGCTAAGGTGG
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ATCATGGAGCTTCACGCAAAGTGGGGAAACAGGTGGTCCAAAATTGCCAAGCATCTACCT
                                                                                                         CTABACTACCTCCGTCCTGATGTTAGAAGAGGGAATATTACACCCGAGGAACAACTTTTG
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Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 314 200 10.2
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
South Memorial Parkway Huntsville, AL 35801 For further information
'^^^1_613-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: '
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Wector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI, The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRWA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GlbcoBRL). This library was constructed in the laboratory of Dr. Randy Sheemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/clone_lib="Gm-c1061"
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BE658316.1
                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Other ESTs: AI930997 corresponding to Gm-c1015-278 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Progra
Soybean (NSF 9872565)
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Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
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Glycine max
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GM700005B10E4 Gm-r1070 Glycine
                                                                                                                                                                                                                                                                                                                                                                                ystems.com web site:www.genomesystems.com Seq primer: 5'-TTTTTTTTTTTTTTTTTTTTTT(A/C/G)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (217) 244-6147
(217) 333-4582
       /cutue_Time library Gm-ri070 is a sequence-driven, reracked /note="The library Gm-ri070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-ri070. The cDNA clones of the reracked Gm-ri070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. A., Director,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-vodkin@uiuc.edu
                                                                                                                                                                                                                                                                    /organism="Glycine max"
/db_xref="taxon:3847"
/clone="Gm-r1070-1759"
/clone_lib="Gm-r1070"
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                                                   GGAAACAGGTGGTCCAAAATTGCCAAGCATCTACCTGGTAGGACAGATAATGAGATCAAG
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript II SK+; Site 1: BcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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/tissue_type="mature flowers of field grown plants"
/lab_host="DH10B"
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1061-4134"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,Y., Person,B., Swaller,T., Gibbons,M., Pape,I,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., R., Waterston,R. and Wilson,R.
Public Soybean EST Project
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BM732539.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shoemaker R/Public Soybean Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK+; Site_1: Consisting of field grown plants for maNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The
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/clone lib="Gm-c1061"
/tissue_type="mature flowers of field grown plants"
/lab_host="DH108"
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                                    Medicago truncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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R., Inman,J.T., Weller,J.W.,
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                                     ATTAATAATCAACTTATAGGAAGCACAAGCCAAATTTCCAACATTGCTGAACCTATGGAC
                                                                                                                     GGAAGAACCGATAATGAGATAAAGAACTACTGGAGGACAAGGATCCAAAAGCATATCAAG
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Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 669 Std Error: 0.00
Plate: 037 row: A column: 10
Seq primer: TCACACAGGAAACAGCTATGAC.
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The Samuel Roberts Noble
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Contact: Harrison MJ
MetTyrSerProProCysTyrGlnGlyMetLeuGluProPheSerThr-----
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/tissue_type="leaf"
/dev_stage="trifoliate"
/dev_stage="trifoliate"
/note="Vector: Lambda Zap; At the trifoliate stage, M.
runcatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."

141 c 127 g 176 t
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/db_xref="taxon:3880"
/clone="NF037A10PL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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NF028G06FL1F1051 Developing flower
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: gdmay@noble.org
Insert Length: 682 Std Err
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Samuel Roberts Noble Foundation
Samuel Roberts Noble Foundation
OK
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580 221 7391
580 221 7380
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                                                                                                                                                                                                /note="vector: Lambda Zap; cDNA was prepared from polyA+enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-poned flowers at flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold
                                                                                                                                                                                                                                                                           /tissue_type="Developing flowers"
/dev_stage="Developmentally pooled. Contains
very young, developing, fully-opened flowers
in early transition into pods."
                                                                                                                     using SOLR cells."
142 c 128 g
                                                                                                                                           packaging extracts. Phagemids containing CDAN inserts were in vivo excised from the recombinant Uni-ZAN XX vector using ExAssist helper phage and the E coli strain XII-Blue MRF' (Stratagene). Excised plasmids were plated
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                                                                                                      Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                       Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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                                                                                                      GlnAla---GluAsnPheGlnGlnGlnSerSerAsnAsnSerGluIleAsnAspHisGln 139
                                                                                                                                                                                           GlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGlnLysHisIleLys 120
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                                                                     CHAGCTTCCAGCAGCAGCAACAGAGTAGTAATTCTGAGATAATTTATCATCCCCAA
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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n quality sequence stop: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI. XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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/clone_lib="Gm-c1061"
/tissue_type="mature flowers of field grown plants"
/lab_host="DH10B"
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public Soybean EST Project
Unpublished (1999)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
seq.primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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523 bp mRNA linear EST 30-NOV-2001 sb45h07.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1015-278 5' similar to TR:Q39028 Q39028 ATMYB2. ;, mRNA
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Location/Qualifiers
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                                                                                                   /note="Wector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

111 g 115 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-278"
/clone_lib="Gm-c1015"
/tissue_type="Mature flowers, field grown plants"
/lab_host="XH10-Gold"
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db_xref="taxon:3847"
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                                                                                                                                                              Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J. Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                     12/2037 688 bp mRNA 1 NF091A12FL1F1088 Developing flower Medicago NF091A12FL 5', mRNA sequence.
                                                                                     Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7391
Fax: 580 221 7380
                      Email: gdmay@noble.org
Insert Length: 688 Std Error: 0.00
Plate: 091 row: A column: 12
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
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/organism="Medicago truncatula"
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AsnTyrTrpSerMetGluAspSerTrpSerMetGlnLeuLeuAsnGlyAsp
                                                                       CAGTTCCCTACAATCTCT---GATCAATCAGGTTGTTCT-------
                                                                                                              GlnPheProThrIleAsnProAspGlnSerSerCysCysThrAsnAspAsnAsnAsnIle
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144 c 125 q
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/dev gtage="Developmentally pooled. Contains a mixture of very young, developmentally fully-opened flowers and flowers in early transition into pods."
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/clone_lib="Developing flower"
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                                                                                                                                                                 No.:
                                                                       Match
                                                                                             Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further i:
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanno,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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Washington University School of Medicine
Washington Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
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                                                                                                                                                                                                                                             /note="Vector: pBluescript II Sk+; Site 1: EcoRI; Site 2: Xhol; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRI). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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/clone="SOYBEAN CLONE ID: Gm-c1061-3735"
/clone_lib="Gm-c1061"
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/lab_host="DH10B"
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 ${\tt MetAspLysGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTrp}$ 

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REFERENCE
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1 (base
                      www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop:
                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Rustlender Ru
                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Conteat: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                                                                                                            ResGen, Invitrogen Corp. 2130
e, AL 35801 For further information
                                                                                                                                 ccu@resgen.com web
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                                                                                        CysTyrGlnGlyMetLeuGluProPheSerThrGlnPheProThrIleAsnProAspGln 178
                                                                                                                                          -----SerThrSerHisValSerThrMetAlaGluProMetGluMetTyrSerProPro 158
                                                                                                                                                                                CAAGCTGAGACTTCACAACAACAT-----GGTAATTCAGAGAATAATGATCATCAAGCA
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                                                                                                                      AGCACTAGTACTAGCAAAGTGTCCACCATGGCACATCCAAATGAGACTTTCTCTCCACCC
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/clone="SOYBEAN CLONE ID: Gm-c1061-3330"
/clone_lib="Gm-c1061"
/clone_lib="Gm-c1061"
/tissue_type="mature flowers of field grown plants"
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                                                                                                                                                                                                                                                  ArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHis
                                                                                                                                             CysArgLeuArgTrpLeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrPro
                                                                                                                                                                                     GGTGAAGGTGTTTGGAACTCTCTAGCTAAATCTGCTGGTCTCAAACGTACTGGAAAAAGT
                                                                                                                                                                                                     GlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSer
GCGAAGCATTTGCCTGGAAGAACGGATAACGAGATAAAAAACTACTGGAGGACTAGGATT
                AlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIle
                                                                                                                          TGTAGACTCCGATGGCTAAATTATCTTCGACCTGATGTCAGGAGGGGGTAATATTACACCT
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Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Hol, Alcala, J., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
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EST244897 tomato ovary,
CLED6E18, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Yector: pBlueScript SK(-); Site 1: EcoR1; Site 2 Xho1; CLED - Tomato Carpel EST Library. OligodT-primed directionally cloned CDNA in vector Lamda ZAP II with and 3' ends located at the EcoRI and XhoI sites, respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="tomato ovary, TAMU"
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/dev stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue_MRF/"
/lab_host="XL1-Blue_MRF/"
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/clone="cLED6E18"
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Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: estewation.wustl.edu
Email: estewation.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 909 Std.Keror: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40RP from Gibco
High quality sequence stop: 4
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 420.
/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by
                                                                                                                                                                                                                       /tissue_type="Mature flowers, field grown plants"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                               /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-8383"
/clone_lib="Gm-c1015"
                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
/db_xref="taxon:3847"
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Search completed: February Job time: 1931 secs

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Ś Ş 밁 S 밁 밁 BASE COUNT ORIGIN 8 멂 Ś Ş 멍 Ś 밁 Ş US-10-021-811-36 (1-206) x BE057370 DB: Percent Similarity: Best Local Similarity: Query Match: Alignment 316 No.: 436 148 376 128 109 256 196 136 89 69 49 76 29 16 9 MetAlaGluProMetGluMetTyrSerProProCysTyr 160 GAAACAGGTGGTCCAAAATTGCCAAGCATCTACCCGGAAGGACTGATAATGAGATTAAG GlyAsnArgTrpSerLysIleAlaLysHisLeuProGlyArgThrAspAsnGluIleLys MetAsnTyrIleAlaAsnHisGlyGluGlyValTrpAsnSerLeuAlaLysAlaAlaGly ATGGCGCAGCCCATAGAAACCTATTCTCCACCCAGTTAT GlnSerSerAsnAsnSerGluIleAsnAspHisGlnAlaSerThrSerHisValSerThr AsnTyrTrpArgThrArgIleGlnLysHisIleLysGlnAla---GluAsnPheGlnGln ArgArgGlyAsnIleThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTrp CTTAAACGTACCGGAAAGAGTTGCCGGCTCCGGTGGCTAAACTACCTCCGTCCTGATGTT LeuLysArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuArgProAspVal ATCACCTATATTGCCAATCACGGGGAAGGGGTTTGGAACTCTTTGGCCAAGGCTGCTGGA ACGTCTCATGATCCTGAAGTGAGAAAGGGGCCATGGACAATGGAAGAAGACTTAATCTTG ThrSerGlnAspProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeu CAGAGTAGTAATTCTGAGATAATTTATCATCCCCAAGCTTGCACTAGCCAAGTGTCCACC AGAAGAGGGAATATTACACCCGAGGAACAGCTTTTGATCATGGAACTTCATGCAAAGTGG 145 ա XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

113 c 116 g 102 t 2.9e-73 709.50 90.85% 86.93% 62.35% (1-476)Length:
Matches:
Conservative:
Mismatches: Gaps: Indels: 474 476 133 6 13 13 435 375 108 195 147 127 315 255 88 8 135 48 75 28

D \$ 맑 Ş 밁 Ş В Ś